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A;Reference number: A75001
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A;Experimental source: strain Orsay
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A;Cross-references: UNIPROT.002038; EMBL:U93075; NID:g1947095; PID:g1947096; PIDN:AACG3009
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein
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R. Jeziorski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V.
J. Biol. Chem. 273, 22792-22799, 1998
A.Title: Cloning and functional expression of a voltage-gated calcium channel alphal A. Reference number: Z22300; MUID:98380510; PMID:9712913
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C;Species: Cyanea capillata
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|207 PEDIKKARKLIVYTSVKGVGDGFISRHINRKISTRISALLVEHVTPNQM-------
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C;Superfamily: Aquifex aeolicus glucose-1-phosphate thymidylyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 YKVIPALRKVPGKRDERIFLIMMLLTLVGWIKALFL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 AKVI -- LSKLFSQGAFGYVLPIISFILAWIETWFL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 KKGISDVRRTFCLFVTFDL-LFVTLLWIJELNVNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match
T.5%; Score 90; DB 2
Local Similarity 23.5%; Pred. No. 7.3;
tes 43; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 FLLAVFRFKVLI -- LAYAV-----CR----
                                                                                                                                                                                                                                                                                                                                                                                         5 PEDMENA-----
                                                                                                     A; Molecule type: DNA
A; Residues: 1-424 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|:
RVL 970
                                                        A;Accession: D75080
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
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                                                                                                                                                                                                                                                                                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein dppB-1 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H902B1
K;Sho, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries; A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H902B1
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: I-348 «KUR»
A;Residues: I-348 «KUR»
C;Genetics:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucose-1-phosphate thymidylyltransferase related protein PAB2433 - Pyrococcus abyssi C;Species: Pyrococcus abyssi C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004 C;Accession: D75080 Rsquence, Genoscope R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 NVNGGIENTLEK-----EVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 TTAVTSAFLLAKVILSKLFSQGAF-GYVLPIISFILAWIETWFLDFKVLPQEAEEENRLL 187
                                                                                                                                                                                                                                                                     EVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKL 146
                                                                                                                                                                                                                                                                                                                                                                   147 FSQGAFGYVLPII-SFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSD 205
                                                                                                                                                                                                                                                                                                                                                                                              ĠSQRIĠVŠKDŘKRFIVITFFDTSITIĹĽMLLCTVTRDDDWDKVFFNĖINI-----FNP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLFVTLLWIIEL 74
                                                                                                                                                                            -----ELNVNGGIENTLEK
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 348;
                                                                              Length 478;
            A;Gene: CESP:F26F4.4
A;Introns: 47/2; 81/2; 125/3; 171/3; 214/1; 236/2; 343/3; 444/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.6%; Score 102.5; DB 2; Length 3 Best Local Similarity 23.7%; Pred. No. 0.066; Matches 49; Conservative 35; Mismatches 66; Indels
                                                                                                                             73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.1%; Score 204; DB 2; Best Local Similarity 26.5%; Pred. No. 2.7e-11; Matches 56; Conservative 36; Mismatches 73
                                                                                                                                                                            GREKKGISDVRRTFCLFVTFDLLFVTLLWII-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOFYSPPESEA -----GSEEAEEKQDSEKP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 IVQDASERAALIPGGLSDGQFYSPPES 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAALAYAVKVFPPGGMTS---VPPPKN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: dppB-1
                                                                                                                                                                                                                                                                                                                         122
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A;Cross-references: UNIPROT:O51531; GB:AE001160; GB:AE000783; NID:g2688505; PIDN:AAB9152.
A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-438 <LER>
A;Residues: 1-438 <LER>
A;Cross-references: UNIPROT:Q13286; GB:U32680; NID:g1039422; PIDN:AAB51075.1; PID:g10394.
                                                                                                                                                                                                                                                                                                                                C;Accession: A57219
R;Lerner, T.J.; Boustany, R.M.N.; Anderson, J.W.; D'Arigo, K.L.; Schlumpf, K.; Buckler, R.Em.; de Vos, N.; van Ommen, G.J.B.; Breuning, M.H.; Doggett, N.A.; Meincke, L.J.; Liu, F.M.O., S.E.
Cell 82, 945-957, 1995
A;Title: Isolation of a novel gene underlying Batten disease, CLN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conserved hypothetical integral membrane protein BB0584 - Lyme disease spirochete C; Species: Borralia burgdorferi (Lyme disease spirochete)
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Somman, C.; Garland, S.; Fujii. C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
R; Fullo: Ganomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 LFVTLLWII------ELNVNGGI-----ENTLEKEVMQYDYYSSYFDIFLLAVFRF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 VFKGLLWYIVPLVVVYFAEYFINQGLFELLFFWNTSLSHAQQYRWYQM---LYQAGVFAS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----WFGF-LPSIYLVFLIILY 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 DTHKYAAYSISFSIYFIIFWIIHSFCISLNIMMGYEMHNSKKEIMKVAIXLSKIGLKLAF 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: G70172
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 DVRRIFCLFVTFDLLFVTL----LWIIELNVNGGIE-NTLEKEVMQYDYYSS-----Y 97
                                                                                                                                                                                                                                 Batten disease-related protein CLN3 - human
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 KVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:120593; OMIM:204200
A;Map postition: 16p12.1-16p11.2
C;Superfamily: CIN3 protein/Battenin/Batten disease protein/BTN1 protein
C;Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary, not compared with conceptual translation A,Molecule type: mRNA
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                               | : |: || | : : || | : : || || BYLEFVACNIE--FKNGRILANLEGKKEGSSAIINNLNNKAALM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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PIISFILAWIETWFLDFKVLPQ-EAEEENRLLIVQDASERAALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 R---SSLRCCRIRFTWALALLOCLNLVFLLADV---
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Best Local Similarity 24.4%; Pred. No. 4;
Matches 47; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
7.2%; Score 85.5; DE
Best Local Similarity 25.5%; Pred. No. 3.5;
Matches 38; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----AWIETWFLDFKVLPQEAEENR 185
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A;Residues: 1-448 <K
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157
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R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin (C;W.; Quali, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Reference number: Ba1299

A;Residues: 1-396 <-Par.
A;Rosidues: 1-396 <-Par.
A;Ro
                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q20170; EMBL:Z68342; PIDN:CAA92775.1; GSPDB:GN00022; CESP:F3
A;Experimental source: clone F38E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:F38E11.7
A;Map position: 4
A;Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --AIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AKNLNCDTRVFPLLKDDEK 225
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                 hypothetical protein F38E11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21969
R;Matthews, P.
Submitted to the EMBL Data Library, January 1996
A;Reference number: Z19495
A;Reference number: Z19495
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: L767 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.2%; Score 86.5; DB 2; Length 767; llarity 24.8%; Pred. No. 5.4; Conservative 22; Mismatches 49; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIFDLLFVTLLWIIELNVNGGIE----NTLEKEVMQYDYYSSYFDI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%; Score 85.5; DB 2;
21.0%; Pred. No. 3.1;
tive 35; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 LGEALENPAQIRSSNHIAIANL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 ISFILAW--IETWFLDFKVLP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 NSDTSSWDGVNATFDDDEYLP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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nes 47; Conserva
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A; Cross-references: UNIPROT: Q8ZDT0; GB: AL590842; PIDN: CAC91281.1; PID: 915980470; GSPDB: GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-590 cMAS>
A;Cres-teferences: UNIDROT:Q34192; EMBL:X56015; NID:g12879; PIDN:CAA39492.1; PID:g12882
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ILSKIFSQGA-----FGYVLPIIS-----FILAWIETW-----FL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 VAYSIVFSKIFSQNGPLNTFLYDWFGFTLPWLTSPDFAMLSIALVVTWKFVGYYGLILFS 176
                                    --YDYYSSYFDIF----LLAVFRFKVL 111
                                                                                                                       112 I-----LAYAVCRLRHWWAIALTTAVTSAF-----LLAKVILSKLFSQGAFGYVLPIIS 160
                                                                                                                                                                                                                      68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
74
---LLFVTLLWIIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 KGISDVRRTFCLFVTFDLFVTLLWIIELNVN------GGIENTL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 KOVGSVLAASYLGYTSIFWFYPFIWLAVLSLTEWRFVGIPTFNGLNNFILVMQDPLFWKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.9%; Score 83; DB Best Local Similarity 22.3%; Pred. No. 3.7; Matches 44; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: inner membrane protein ugpA
                                                                                                    75 NVNGGI-----ENTLEKEVMQ-----
    38 ESYEGREKKGISDVRRTFCLFVTFD-
                                                                                                                                                                                                                                                                                                                 ||::|::|::|
277 LILSLVGGTFINYKIMPE 294
                                                                                                                                                                                                                                                                                        161 FILAWIETWFLDFKVLPQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFKVLPQE----AEEEN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLNSIPKEIYSAAELDN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-291 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Genetics:
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                                                                                                                                                                                                                                                                                                                                                                      integral membrane protein pssA - Chinese hamster
(C.Species: Cricetulus griseus (Chinese hamster)
(C.Species: Cricetulus griseus (Chinese hamster)
(C.Species: Orlo-1992 #sequence_revision 30-Jun-1992 #text_change 06-Oct-2000
(C.Accession: A41680
(R.Kuge, O.: Nishijina, M.; Akamatsu, Y.)
(A. Biol. Chem. 266, 24184-24189, 1991
(A. Reference number: A41680; MUID:92084729; PMID:1748687
(A.Accession: A41680
(A.Status: preliminary
(A.Molecule type: mRNA)
(A.Status: Dreliminary
(A.Molecule type: mRNA)
(A.Status: Caenores: GB:D10234; GB:D90468; NID:g220280; PIDN:BAA01084.1; PID:d1001553; PIC:Superfamily: Caenorhabditis elegans hypothetical protein ZC506.3
(C.Superfamily: Caenorhabditis elegans hypothetical protein ZC506.3
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-----FMHLLP--NF 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DYYSSYFDIFLLAV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 F----REKVLILAYAVCRLRHWMAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISF 161
                                                               151
                                                                                                                            -----FGYVLPIISFILAMIETWFLDFKVLPQEAEEENRLLIV-----QDASERAA 197
                                                                                                                                                  390 GAIMEGSVIFVYIIP-IAFVLA-----NYTNLPFE-----IIVFIPSLEDAIKLVV 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                    98 FDIFLLAVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVI--LSKLFSQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75;
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7.0%; Score 83.5; DB 2;
Best Local Similarity 19.2%; Pred. No. 4.1;
Matches 38; Conservative 35; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 7.1%; Score 84.5; DB 2; Similarity 24.4%; Pred. No. 4.7; 32; Conservative 22; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 FCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :| :| :| :| :| 173 FWGWAMKALLIRSYGLC----WTISITWELTELF-
                                                                                                                                                                                                                              198 LIPGGLSDGQFYS 210
                                                                                                                                                                                                                                                                          -----YFYS 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 ILAWIETWFLD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AECWWDQVILD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 32; Conserva
                                                                                                                                                                                                                                                                          SLP
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A;Residues: 1-239 <TIGR>
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164227

hypothetical protein homolog MG247 - Mycoplasma genitalium

C;64227

hypothetical protein homolog MG247 - Mycoplasma genitalium

C;5Accessian: C6-227

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Datesion: C6-227

R;Fraest C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;

M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.C.A.; Venter, J.C.

Science 270, 397-403, 1995

A;Title: The minimal gene complement of Mycoplasma genitalium.

A;Reference number: A64200; MUID: 96026346; PMID: 7569993

A;Accession: C64227

A;Accession: C64227

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A;Accession: C6227

A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tras protein - Escherichia coli plasmid pED208
C.Species: Escherichia coli
C.Species: Bacherichia coli
C.Date: 04-Aug-1988 #sequence_revision 04-Aug-1988 #text_change 09-Jul-2004
C.Jacession: B29835
R.Pinlay, B.B.; Paranchych, W.
J. Bacteriol. 166, 713-721, 1986
A.Title: Nucleotide sequence of the surface exclusion genes tras and traT from the IncP-A.Reference number: A29835; MUID:86223783; PMID:3011738
                         A;Genome: mitochondrion
A;Genetic code: 8GC6
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                              55 FCLFVTF-----DLL---FVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVF 106
                                                                                                                                                                                                                                                                                                                 61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLL----AVFRFKVLILAY 115
                                                                                                                                                                                                                                                                                                                                                                                         107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWI 166
                                                                                                                                                                                                                                                                                                                                                                                                                        116 AVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPII-----SFILAW 165
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                                                                                                                                                                 Query Match 6.9%; Score 83; DB 1; Length 590; Best Local Similarity 23.9%; Pred. No. 8.4; Matches 32; Conservative 23; Mismatches 37; Indels
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C;Genetics:
A;Genome: plasmid
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144 GFSWFVTYLI 153
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A;Molecule type: DNA
A:Residues: 1-186 <FIN>
A; Gene: ND5
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5.1.6 Compugen Ltd.		, Search time 193 Seconds (without alignments) 597.604 Million cell updates/sec	. EAGSBEAEBKQDSEKPLLEL 234		81	ers: 1825181				cted by chance to have a coft to compare the result being printed,		Description	100	Q9acıs mus musculu Q6disB brachydanio O6dfr7 xenomus fro	Q6pf40 xenopus lae Aah57738 xenopus l	Q6gnt3 xenopus lae Q14849 homo sapien	Aap35610 homo sapi Q61542 mus musculu	Bac30977 mus muscu Q6ph03 brachydanio	Aah56766 brachydan Q8bmp8 m mus muscu	Q7qit3 anopheles g O8mzh4 drosophila	Aas64770 drosophil	Agrily Cooppil	Aal4/232 urosophii Q19819 caenorhabdi		Q9uzw1 pyrococcus Q8hq10 thrips imag	strepto helicok	005	V/III) 1 NYCOPIASHA 002038 cyanea capi
GenCore version 5. Copyright (c) 1993 - 2005 Co	OM protein - protein search, using sw model	Run on: January 24, 2005, 16:04:45 ; Se (wit 697.	Title: US-10-063-518-14 Perfect score: 1195 Sequence: 1 MMHLPEDMENALTGSQSSHA	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	egs,	Total number of hits satisfying chosen paramete	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1500 summaries	02:* rot_sprot:* rot_trembl:*	s the number of results predier than or equal to the score wed by analysis of the toral	SUMMARIES	Result Query No. Score Match Length DB ID	1195 100.0 234 1 MENT	1134:5 54:9 235 1 MENI MOUS 796 66:6 227 2 Q6DI38 700:5 58:6 448 2 O6DFR7	698.5 58.5 444 2 698.5 58.5 444 2	684 57.2 448 2 664 55.6 445 1	664 55.6 445 2 656.5 54.9 446 1	656.5 54.9 446 632 52.9 448	632 52.9 448 2 492 41.2 107 2	348 29.1 568 343 28.7 545	343 28.7 545 2 343 28.7 583 2	343 28.7 583 2	204 17.1 447 2	102.5 8.6 348 2	93.5 7.8 424 2 93.5 7.8 564 2	91 7.6 246 2 91 7.6 525 2	.6 651 2	90 7.5 1911

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 | 07a6d3 staphylococ | Q6qfb9 legionella | Q6qfc5 legionella | Qeqtc7 legionella | Associate regioneri | Aas92187 legionell | Q9ceg6 lactococcus | Q8rbz7 thermoanaer | Ografi Streptomijes | 023384 arabidopsis | Q9evj7 flavobacter | Q6m052 methanococc | Catzyy/s methanoco
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Schnerch A., Schein J.E., Jones S.J.M., marra M.A.,
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MEDLINE-2138257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RC STRAIN=CS7BL/6J; TISSUB=Cerebellum, and Kidney;

RR MEDLINE=2534683; DubMed=12466851; DOI=10.1038/nature01266;

RR MEDLINE=2534683; PubMed=12466851; DOI=10.1038/nature01266;

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-!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-UDL-2004 (Rel. 44, Last annotation update)
MLN64 N-cerminal domain homolog (STARD3 N-terminal like protein)
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IsoId=Q9DCI3-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                           Name=Stard3nl; Synonyms=Mentho;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                        (Mouse)
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                                                                                                                                                                                                                                                                                   Mus musculus
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and mouse
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDLLEVTLLAVIELNVNGGIENTLKKEVIHYDYSSSYFDIFLLAVFRPKVLILGYAVCRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNHLPBEHMENTLTGSQSSHASLRDIHSINPAQLMARIESYEGREKKGISDVRRTFCLFVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).
SEBEAEBKQESEKPLLEL -> RNSSAFRMGIQKSSQPSGG
AAGTRARFVPKASSCREGRPGLPMWLQ (in isoform
              Note=No experimental confirmation available;
SMILIARITY: Contains 1 MENTAL domain.
CAUTION: Ref.1 (BAB31166) sequence differs from that shown due to
a frameshift in position 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGS-EEAEEKQDSEKPLLEL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٦;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1134.5; DB 1; Length 235; Pred. No. 9.5e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP_003909.
QL -> HS (in Ref. 1; BAB22337).
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F251725390CB1503 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic (Potential).
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
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01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
IsoId=Q9DCI3-2; Sequence=VSP 003909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
                                                                                                                                                                                                                                                                            EMBL; AK002760; BAB22337.1; -.
EMBL; AK018331; BAB31166.1; ALT_FRAME.
EMBL; BC003334; AAH03334.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   Potential
                                                                                                                                                                                                                                                                                                                                                            Alternative splicing; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26811 MW;
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74
97
118
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52
235 AA;
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NCBI_TaxID=7955;
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144
151
172
218
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CONFLICT
SEQUENCE
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TRANSMEM
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TRANSMEM
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Q6D138;
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06D138
1D 06D138
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robark S.A., McEwan P.J., McKernan R.J., Malke J.A., Gunazane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIA 127
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1-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Everopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 227 AA; 25485 MW; 24C46AD8FF4985C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 66.6%; Score 796; DB 2, Best Local Similarity 68.3%; Pred. No. Se-64; Matches 155; Conservative 31; Mismatches 3
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUL-2004) to the
EMBL; BC075752; AAH75752.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences.";
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SEQUENCE
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AAH57738
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bromstein M.J., Usdin T.B., Toshiyuti S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Wilalahon D.K., Muzuy D.M., Sodergren B.J., Lu K., Gabbs R.A., Wilalahon D.K., Muzuy D.M., Sodergren B.J., Lu K., Gabbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., A Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S., Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Radinan and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 IVRLRHWWAIAITTLVTSAFLIAKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 VCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVL 176
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H.S., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max. S. I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters M.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGC68989 protein.
Kenopus laevis (African clawed frog).
Eukaryosa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 448;
                                                                                                                                                                                                                                                                                                                                                       58.6%; Score 700.5; DB 2; Length 4 61.1%; Pred. No. 5.3e-55; ive 29; Mismatches 49; Indels
                                                                                                                                                                                                                                                                    Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC076666; AAH76666.1; -.
                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 448 AA; 50926 MW; 2686D07C737D4204 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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MEDLINE-22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                   cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 61.13
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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05-JUL-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Best Local 6
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FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Bakesley R.W., Youchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Cranīata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S., Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057738; AAH57738.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FART; 1.
50572 MW; 7BEA97317BF48358 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.5%; Score 698.5; DB 2; 60.9%; Pred. No. 7.9e-55;
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02-MAR-2004 (TrEMBLrel, 27, Last seqn
02-MAR-2004 (TrEMBLrel, 27, Last anno
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Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22341132; PubMed=12454917;
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SMART; SM00234; START; 1.
PROSITE; PS50848; START; 1.
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Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dev. Dyn. 225:384-391(2002)
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InterPro; IPR002913; START.
Pfam; PF01852; START; 1.
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initiative.
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carannor T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broask S.A., McKennan N.J., Marke J.A., Gubbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevychenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Norley W., Marra M.J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDLLFVTLLWIIELMVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRL 120
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Hypothetical protein.

Energy a laevis (African clawed frog).

Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Buteleostomi;

Amphibia: Batrachia; Annra: Mesobatrachia; Pipoidea; Pipidae;
Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057738; AAH57738.1; -. SEQUENCE 444 AA; 50572 MW; 7BEA97317BF48358 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                         MEDLINE=22388257; PubMed=12477932;
                                            Dev. Dyn. 225:384-391 (2002).
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                            SEQUENCE FROM N.A.
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                           initiative.
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Jones S.J., Marra M.A.,

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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
MLN 64 protein (StAR-related lipid transfer protein 3) (StARD3) (START
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MTKLPGEFOPDLERSLPAIASINSSMSHNHVPSPHSLLPR-----EQRRLISDVRRTFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ll protein.
448 AA; 51279 MW; 472FF8BTC3B2F5E4 CRC64;
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PRINTS; PR00978; STARPROTEIN.
SMART; SM00234; START; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev. Dyn. 225:384-391(2002).
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InterPro; IPR000799; StAR.
InterPro; IPR002913; START.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences."
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Matches 139; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q -> R (in Ref. 3; AAH08356/AAH25679).
G -> A (in Ref. 3; AAH25679).
                                                                                                                                                                                                                                                                                                                                                     SWART; SM00234; START; 1.
PROSITE; PS50848; START; 1.
3D-structure; Lipid transport; Lipid-binding; Steroidogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extracellular (Potential)
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                                                                                                                                                                                                                                MIM; 607048; -.
GO; GO:000573; C:cytoplasm; TAS.
GO; GO:0005203; P:cholesterol metabolism; TAS.
GO; GO:0006839; P:mitochondrial transport; TAS.
GO; GO:0008202; P:steroid metabolism; TAS.
InterPro; IPR000799; SLAR.
InterPro; IPR0002913; STARI.
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EMBL; D38255; BAA22525.1; -.
EMBL; BC008356; AAH08356.1; -.
EMBL; BC008747; AAH08747.1; -.
EMBL; BC025679; AAH08747.1; -.
                                                                                                                                                                                                                                                                                                                            Pfam; PF01852; START; 1.
PRINTS; PR00978; STARPROTEIN.
                                                                                                                                                                                                  PDB; 1EM2; X-ray; A=216-444.
Genew; HGNC:17579; STARD3.
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DOMAIN 1 51
TRANSMEM 52 72
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72
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PDB; 1EM2; X-ray; A
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        membrane protein.
SIMILARITY: Contains 1 MENTAL domain.
SIMILARITY: Contains 1 START domain.
SIMILARITY: Contains 1 START domain.
DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW-"http://www.infobiogen.fr/services/chromcancer/Genes/MLN64ID202.html".
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X REDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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B Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

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"Generation and initial analysis of more than 15,000 full-length human
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MEDLINE=97413641; PubMed=9270027;
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"Isolation of a candidate gene, CABI, for cholesterol transport to
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method.";
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Nat. Struct. Biol. 7:408-414(2000).
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-I. FUNCTION: Binds and transports cholesterol. Promotes steroidogenesis in placenta and brain.

-I. SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=20264523; PubMed=10802740;
          (CAB1 protein).
                       Name=STARD3; Synonyms=MLN64, CAB1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                           Cancer Res. 57:3548-3553(1997).
          domain-containing protein 3)
                                                                                                                                                                                                                   Genomics 28:367-376(1995).
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                                                                             NCBI_TaxID=9606;
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05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                              DFKVLPQEAEEERWYLAAQVAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVAGKK 229
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                                                                                                                                          ILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
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                                                            1 MNHLP----EDMENAL----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV
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                                        Gaps
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                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                               Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                        22;
                   Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.6%; Score 664; DB 2; Length 445; 56.2%; Pred. No. 1.1e-51; live 38; Mismatches 45; Indels 3
                  ; Score 664; DB 1; Length 445; Pred. No. 1.1e-51; 38; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BT006964; AAP35610.1; -. SEQUENCE 445 AA; 50474 MW; 62BED5C3EDA0DDEF CRC64;
62BED5C3EDA0DDEF CRC64;
                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Q61542;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                         Created)
50474 MW;
                   55.6%;
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                                                                                                                                                                                                                                                                                                     START domain containing 3. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 56.24
Matches 135; Conservative
                              al Similarity 56.2
135; Conservative
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 445 AA;
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AAP35610;
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ID ML64 MC
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Considerable Statement Sta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
MLN 64 protein (StAR related lipid transfer protein 3) (StARD3) (START domain-containing protein 3) (ES 64 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96039245; PubMed=7490069; Tomasetto C., Regnier C.H., Moog-Lutz C., Mattel M.-G., Chenard M.-P., Lidereau R., Basset P., Rio M.-C.; Inidereau R., Basset P., Rio M.-C.; Indertification of four novel human genes amplified and overexpressed in breast carcinoma and localized to the q11-q21.3 region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Binds and transports cholesterol. Promotes
steroidogenesis in placenta and brain (By similarity).
-!- SUBCELULAR LOCATION: Integral membrane protein. Late endosomal
embrane protein (By similarity).
-!- SIMILARITY: Contains 1 MENTAL domain.
-!- SIMILARITY: Contains 1 START domain.
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Lipid transport; Lipid-binding; Steroidogenesis; Transmembrane;
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Extracellular (Potential).
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                                                                                                           Name=Stard3; Synonyms=Mln64, Es64;
Mus musculus (Mouse).
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MGD; MGI:1929618; Stard3.
InterPro; IPR000799; STAR.
InterPro; IPR002913; START.
Pfam; PF01852; START: 1.
PRINTS; PR00978; STARPGTEIN.
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STRAIN=AB; TISSUE=Whole body;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Thymus;
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NCBI_TaxID=7955;
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SEQUENCE FROM N.A.
STRANT=C57BL/6J; TISSUB=Thymus;
MEDLINE=223546683; PubMed=12466851;
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
MARAPISE of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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SECUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Thymus;
MEDLINE=20499374; Pubmed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                                                                                                               HWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-ARR-2004 (TTEMBLrel. 27, Created)
14-ARR-2004 (TTEMBLrel. 27, Last sequence update)
14-ARR-2004 (TTEMBLrel. 27, Last annotation update)
3 days neonate thymus cDNA, RIKEN full-length enriched library, clone: A630020B16 product:steroidogenic acute regulatory protein
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                                                                                                                                                                                                             17;
                                                                                                                                                                      DB 1; Length 446;
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                     Extracellular (Potential).
                                                                                                                              DBF4359604F3E1E2 CRC64;
                                                           Cytoplasmic (Potential). MENTAL.
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57.8%; Pred. No. 5.2e-51;
ive 33; Mismatches 47
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
Hath-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
    Potential
                                            Potential
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MEDLINE-21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
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                                                                                                                              50469 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Onno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Shiraki T., Sogaba Y., Tagami M., A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogawa P., Tagami M., A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Lomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., EMBL, AKO41538; BAC30977.1:

B. Submitted (Jul. 2001) to the EMBL/GenBank/DDBJ databases.

B. SEQUENCE 446 AA, 50469 MW, DBF4359604F3BIEZ CRC64;
prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                      MEDLINE-20530913; PubMed=11076861; MEDLINE-20530913; PubMed=11076861; MEDLINE-20530913; PubMed=11076861; MEDLINE-20530913; PubMed=11076861; MEDLINE-20530913; PubMed=11076861; Median A., Aizawa K., Naqoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi X., Kitsunai T., Tashiro H., Itoh M., Yamamoco R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Isawa M., Ohara E., Watshiwagi K., Fujiwake S., Inoue K., Tanaka T., Matsuura S., Kawai J., Roneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Last annotation update)
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Haich F.,
A stapleron M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tonahlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
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STRAIR=AB; TISSUB=Whole body;
STRAIR=AB; TISSUB=Whole body;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO566; AAH557661; -.
InterPro; IPR000799; StAR.
InterPro; IPR002913; START.
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448 AA; 50751 MW; 716A18C127B59C5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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STRAIN=AB; TISSUE=Whole body;
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PRINTS; PRO0978; STARPROTEIN.
SMART; SMO0234; START; 1.
PROSTIE; PSS0848; START; 1.
SEQUENCE 448 AA; 50751 WW;
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Matches 127; Conservative
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NCBI_TaxID=7955;
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AC AAH56
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DT 01-AP
DT 01-AP
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Prange C.,
Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse CDNA sequences"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFIL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWIETWFLDFKVLPQEAEEEN-RLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSEE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 BKKGISDVRRIFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLL
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus adult male pituitary gland cDNA, RIKEN full-length
Mus musculus adult male pituitary gland cDNA, RIKEN full-length
(UNKNOWN) (PROTEIN FOR MGC:14607) (SIMILAR TÖ STEROIDOGENIC ACUTE
REGULATORY PROTEIN RELATED) homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.9%; Score 632; DB 2; Length 448; Best Local Similarity 70.9%; Pred. No. 8.7e-49; Matches 127; Conservative 18; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056766; AAH56766.1;
                                                                                                                                                                                                                                                                                                                                                                                                                              1766; AAH56766.1; -.
448 AA; 50751 MW; 716A18C127B59C5D CRC64;
                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/6J; TISSUB=Pituitary gland; MEDLINE=9279253; PubMed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Pituitary gland; MEDLINE=21085660; PubMed=11217851;
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SEQUENCE FROM N.A.
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STRAIN=C57BL/6J; TISSUE=Pituitary gland;
A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A Adachi J., Aizawa K., Akimura T., Harana T., Harbizume W.,
A Fukuda S., Furuno M., Hanagaki T., Harana T., Hirozane T.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Okaato N., Okaato N., Sano H.,
A Saito R., Saitoh H., Sakai C., Sakai K., Saka
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUE=Pituitary gland;

X MEDLINE=C57BL/6J; TISSUE=Pituitary gland;

X Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

A Shibata K., Itoh M., Nakamura K., Nighine T., Harada A.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare fiull-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
[1]
                    the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-673(2002).
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1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
AgCP3158 (Fragment).
Name=agCG52468; ORFNames=ENSANGG0000018959;
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                                                                                           -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 568;
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                                             Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                      preliminary data.

BMBL, AAABO10088077, ERA03945.1; --
GO, GO:0015485, P:cholesterol binding; IEA.
GO, GO:0017127; P:cholesterol transporter activity; IEA.
GO, GO:0006694; P:sterologibiosynthesis; IEA.
InterPro; IPR00799; StAR.
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PRINTS; PR00978; START; 1.
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Search completed: January 24, 2005, 16:18:38

Sequence Sequence Sequence B

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7 US-10-491-056-20

8 US-10-262-839-82

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9 US-10-282-112A-6946

1 US-10-282-112A-6948

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10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   10.000   1	-179 171 171 171 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 179 -	3-803 3-803 3-803 3-803 3-803	3-803 3-990 3-241 3-270 3-270 1-68-2	9-252 9-252 9-328 9-489 8-158 8-811	9-27C	9-09-160 9-00-160 9-89-00-160 9-25-69-25-69-17-17-17-17-17-17-17-17-17-17-17-17-17-	2 8 8 8 8 8 9 1 3 1 8 1 3 1 8 1 8 1 8 1 8 1 8 1 8 1 8	18 - 42 - 42 - 42 - 42 - 42 - 42 - 42 - 4
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1875   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878   1878	121612464	***	H 0 W 4 4 0 W 4	* 4 4 4 4 1 1 1 1 1 1 1	14444666	M 4 2 M H H M 2 M F	4444000000	. ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
1,250   1,250   1,250   1,250   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,500   2,50								
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1488 58.5 4.9 503 3 US-09-134-001C-3096 Sequence 3096, Ap 1489 58.5 4.9 506 4 US-09-436-063C-15 Sequence 15, Appl 1490 58.5 4.9 506 4 US-09-436-063C-15 Sequence 15, Appl 1491 58.5 4.9 510 3 US-08-508-761B-4 Sequence 15, Appl 1492 58.5 4.9 521 4 US-09-10-279-532 Sequence 351, Appl 1494 58.5 4.9 523 4 US-09-134-001C-3514 Sequence 2, Appl 1494 58.5 4.9 533 4 US-09-134-01C-3514 Sequence 2, Appl 1495 58.5 4.9 560 3 US-09-28-352-605 Sequence 2, Appl 1497 58.5 4.9 560 3 US-09-28-352-605 Sequence 4343, Appl 1497 58.5 4.9 607 1 US-07-959-943-7 Sequence 7, Appli 1499 58.5 4.9 607 1 US-07-959-943-7 Sequence 7, Appli 1500 58.5 4.9 630 1 US-07-959-943-9 Sequence 9, Appli 1500 58.5 4.9 633 4 US-09-959-943-9 Sequence 13729, Appli 1500 58.5 58.5 58.5 59.9 633 4 US-09-959-943-9 Sequence 13729, Appli 1500 58.5 58.5 58.5 59.9 633 4 US-09-959-943-9 Sequence 13729, Appli 1500 58.5 58.5 59.9 633 4 US-09-959-943-9	ALICOMMENTS  O8691814B  hristine atherine fer lated Nucleic Acid Molecules Useful Leukemia Markers and in Breast Cancer Prognosis 4  seler, Goldstein & Fox P.L.L.C. Ave, NW, Suite 600  1sk atible DOS/MS-DOS 1ease #1.0, Version #1.30  \$\frac{5}{2}\text{60}\text{602},183  \$\frac{5}{2}\text{60}\text{602},183  \$\frac{5}{2}\text{60}\text{604}; \text{DB 2}; \text{Length 445};  \$\frac{6}{2}\text{7}; \text{Pred}; \text{No. 7e-68};  \$\frac{6}{2}\text{7}; \text{Pred}; \text{No. 7e-68};  \$\frac{6}{2}\text{7}; \text{Pred}; \text{No. 7e-68};	itive 38 MENAL  : : ; NLERSLPAVE
Sequence 20, Appl Sequence 17, Appl Sequence 2, Appli Patent No. 5240846 Sequence 4, Appli Sequence 23345, A Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 39754, A Sequence 5, Appli	acunante e cumante e comente e comen	ednence ednence ednence ednence ednence
US-09-425-453A-20 US-08-469-630-17 PCT-US93-11667-2 5240846-5 12.09-621-92A-4 US-09-621-96A-23345 US-09-248-796A-23345 US-09-273-138-2 US-08-409-373B-2 US-08-621-018B-2 US-09-483-665-2 US-09-270-767-39754 US-09-270-767-5971	US-09-461-912A-44 US-09-461-912A-44 US-09-621-976-5111 US-09-270-767-37959 US-09-270-767-37959 US-09-270-767-37959 US-09-270-767-37959 US-09-134-000C-6287 US-09-134-000C-6287 US-09-134-000C-6287 US-09-134-000C-6287 US-09-134-000C-6287 US-09-134-000C-6287 US-09-134-000C-6287 US-09-134-000C-6287 US-09-134-000C-6287 US-09-134-000C-3458 US-09-134-001C-3433 US-09-134-001C-3433 US-09-134-001C-3433 US-09-134-001C-3458 US-09-134-001C-3448 US-09-134-001C-3448 US-09-134-001C-3448 US-09-134-001C-3448 US-09-134-001C-34412 US-09-243-681A-7965 US-09-243-681A-7965 US-09-243-681A-7965 US-09-243-681A-7965 US-09-243-681A-19135 US-09-243-681A-19135 US-09-27-6506 US-09-27-67-67-67-67-67-67-67-67-67-67-67-67-67	US-09-292-069A-31 US-09-767-013-31 US-09-292-072-31 US-09-198-452A-763 US-09-627-650B-14 US-09-436-063C-14 US-09-792-024-65
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227 LSCYVLEETSV-----MLAKRPLITKPEVISVMKRRIEEICMKVFAQ-----YILGADPLR 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 LWIIELNVNGGIENTLEKEVMQYDY-----YSSYFDIFLLAVFRFKVLILAYAVCRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 L.------TTCVETMCNEYKVTSDACMMTMYGGISLLSEF------CRV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RHWWAIALTTAVTSAFLLAK----- 156
                                                          111 LILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKL----FSQGAFGYVLPIISF---IL 163
                                                                                                                                                                                                                                                                                                                                                                                                         Cytomegalovirus DNA Constructs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 GSQSSHASLRNIHSINPTQLMARIESY-----EGREKKGISDVRRTFCLFVTFDLLFVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 19.3%; Pred. No. 1.6;
Matches 52; Conservative 36; Mismatches 67; Indels 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PREADILE FC-DOS/MS-DOS
SOFTWARE: PATABLI Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 19-Jan-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                  Sequence 4, Application US/09171699
Patent No. 6448389
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of, Anatomy & Biology
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION UNMERS: US 60/015,717
FILING DATE: 23-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Carby A.
REGISTRATION NUMBER: 33,980
REFERRANCE/DOCKET NUMBER: WST66APCT
  15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-171-699-4
                                                                                                                                                                                                                                                                                                                                                     Gonczol, Eva
Berencsi, Klara
Kari, Csaba
TITLE OF INVENTION: No. 6448389el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 406 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
    21; Conservative
                                                                                                                                                          :|: ::
141 SWLPSY 146
                                                                                                                              164 AWIETW 169
                                                                                                                                                                                                                                                         US-09-171-699-4
        Matches
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILLE REFERENCE: 2709-2004001
CURRENT PILLE REFERENCE: 2709-2004001
CURRENT FILLE RAPPLICATION NUMBER: US/09/489,039A
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                               Sequence 92, Application US/08846762A

Sequence 92, Application US/08846762A

Requence 92, Application US/08846762A

Remain Sequence 92, Application US/08846762A

Remain Sequence 92, Application Sequence 92, Applicant Description Sequence 92, Applicant Description Sequence 92, Applicant Description Sequence 93, Applicant Charter, Deborah Applicant General, Teresa TITLE OF INVENTION: No. 5944072el Proteins Involved in the Synthesis and Assembly TITLE OF INVENTION: Of O-Antigen in Pseudomonas Aeruginosa TITLE OF INVENTION NUMBER: US/08/846,762A

CURRENT FILING DATE: 1997-04-30

NUMBER OF SEQ ID NOS: 100

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 GISDVRATFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 GWIDTREFFCWLILLGLFIVDATWTLVRRVLGGFK-----VYEAHRSHG--YQIASR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
                                                                                             DPKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-BAEEKQDSEK 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
6.9%; Score 82.5; DB 2; Length 341;
Best Local Similarity 24.0%; Pred. No. 0.57;
Matches 31; Conservative 20; Mismatches 51; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9711, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION: APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-08-846-762-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.7%;
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SEQ ID NO 9711
LENGTH: 350
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Best Local Similarity
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                                                                                                                                                                                                                                                                    RESULT 2
IIS-08-846-762-92
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SPVPATIPLSSVIVAENSDQEESEQSDEEE 350
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6.6%; Score 78.5; Di
Best Local Similarity 22.5%; Pred. No. 0.9;
Matches 38; Conservative 33; Mismatches
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                                                                                             Sequence 503, Application US/09976594 Patent No. 6673549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 18.0%
Matches 34; Conservative
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ORGANISM: Homo sapiens
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                                                        RESULT 6
US-09-976-594-503
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LENGTH: 221
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                                      ---PIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 LWIIELNVNGGIENTLEKEVMQYDY-----YSSYFDIFLLAVFRFKVLILAYAVCRL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VILSKLFSQGAFGYVL----- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 ---PIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 GSQSSHASLRNIHSINPTQLMARIESY-----EGREKKGISDVRRTFCLFVTFDLLFVTL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.7%; Score 79.5; DB 5; Length 406; Best Local Similarity 19.3%; Pred. No. 1.6; Matches 52; Conservative 36; Mismatches 67; Indels 11
                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9402107
GENERAL INFORMATION:
GENERAL THE WISTER THE WISTER OF, Anatomy and Biology
TITLE OF INVENTION: Recombinant Cytomegalovirus Vaccine
NUMBER OF SEQUENCES:
CORRESPONDENCES.
ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                    STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19477

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02107
                                                                                                                       | :| |: | |:
321 SPVPATIPLSSVIVAENSDQEESEQSDEEE 350
                                                                                               --EAGSEEAEEKQDSEK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---EAGSEEAEEKQDSEK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/017,130
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST6BPCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-540-5200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RHWWAIALTTAVTSAFLLAK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                      278 VCSPSVD-
                                                                                             214 S-----
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GENERAL INFORMATION:
APPLICANT: PUTNESS, Michael
APPLICANT: Burchinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
TITLE OF INVENTION: GENES EXPRESSED
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR PAPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SSO ID NO 503
LENGTH: 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 VAKNSALGPRRLRASWLVISLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFVWTY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLI---- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GAFGY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 VLPIISFILAWIETWFLDFKVLPQEAEBENRLLIVQDASERAALIPGGLSDGQFY---- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LSTVRPGTQ--ALEPGAATEAEGFPGSGR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 CLFVTFDL---LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41033, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT HOMBURGE et al.
; TILLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.7%; Score 79.5; DB 4; Length 723;
18.0%; Pred. No. 3.7;
tive 40; Mismatches 58; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6%; Score 78.5; DB 4; Length 221; 22.5%; Pred. No. 0.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID No. 6673549 2246292CD1
US-09-976-594-503
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123 WWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEABE 182
                                                                       63 LLFVTLLWIJELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 TASISVILLTELG------ DKTFFIAAIMAMRHPRLIVFGGAIA--- 141
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Sequence 43373, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT PELING NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 43373

LENGTH: 251
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Patent No. 6448375

Patent No. 6448375

GENERAL INFORMATION:
APPLICANT: PARMENTIEN:
APPLICANT: PARMENTIEN:
APPLICANT: PARMENTIEN:
APPLICANT: PARMENTIEN:
APPLICANT: PARMENTIEN:
APPLICANT: APPLICANT: PARMENTIEN:
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PEDMENAL - TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFD
                                             63 LLFVTL-----LWIIBLNVN---GGIENTLEKEVMQYDYYSSYF-----DIFLLAVF
                                                                                                                                        107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISF----
Gaps
32;
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18.8%; Pred. No. 1.2;
tive 46; Mismatches 63; Indels
  Indels
  49;
                                                                                                                                                                                                                                   162 ILAWIETWFLDFKVLP---OEAEEE 183
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203 LLATKQNSYFTLPVIPLPGSEAKQE 227
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    32;
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       32; Conservative
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Matches 34; Conserv
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US-09-270-767-43373
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         Matches
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Facera No. 6747137

GENERAL INFORMATION:
FAPPLICATURT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 VVYFCCSFCTTYQLIQGTYNSINFRFNLKNLSLT-----LGFLISPPISIHFSYLPHY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 LAYAVCRLRHWWAIALTT--AVTSAFLLAKVILSKLFSQGAFGYVL-PIISFILAWIETW 169
                                                                          113 LAYAVCRLRHWWAIALTT--AVTSAFLLAKVILSKLFSQGAFGYVL-PIISFILAWIETW 169
                                                                                                                       77 VVYFCCSFCTTYQLIQGTYNSINFRFNLKNLSLT-----LGFLISPPISIHFSYLPHY 129
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       17 CIYIYSSMDQFLFIIILLILLILLTCLSFVEXYLFVNILXIDNYIGNXNVFLFFLLLFQXII 76
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 CLEVIFDL---LEVILLMIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 FLDFKVLPQEAEEENRLL------IVQDASERAAL--IPGGLSDGQF 208
                                                                                                                                                                         170 FLDFKVLPQEAEEENRLL-----IVQDASERAAL--IPGGLSDGQF 208
                                                                                                                                                                                                                130 LVNNSVLHLKNVXIQEFLDXVVKCFFFILRASFRFCLKDIPNGL--GQF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.6%; Score 78.5; DB 4; Length 221; Best Local Similarity 22.5%; Pred. No. 0.9; Matches 38; Conservative 33; Mismatches 73; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Xaa means any amino acid US-09-270-767-56249
                                                                                                                                                                                                                                                                                                                  US-09-270-767-56249
Sequence 56249, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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SEQ ID NO 20444
LENGTH: 228
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Best Local Similarity
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LENGTH: 221
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLLFIFTLPFWIDYKLKDDWVFGDAMCKIISGFYÝTGLÝSEIFFILLTIDRYLAIVHAV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 AVCRLRH------LAKVILSK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 ALKLNLFGLVLPLLVMIICYIGI----IKILLRRPNEKKSKAVRLIFV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 LFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAEEEN----RLLIV 189
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.5%; Score 78; DB 4; Length 355; Best Local Similarity 23.2%; Pred. No. 2; Matches 39; Conservative 25; Mismatches 60; Indels
                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFRENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09938719
Patent No. 6692938
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: No. 6448375e
US-08-833-752-9
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COMPUTER READABLE FORM:
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US-09-938-719-9
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62 DLLFVTLL--WI-IELNVNGGIENTLEKEVMQYDY---YSSYFDIFLLAVFRFKVLILAY 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Indels
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RECEPTORS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Diskette
COMPUTER: DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.5%; Score 78; DB 4
23.2%; Pred. No. 2;
tive 25; Mismatches
REFERENCE/DOCKET NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: NO. 6692938e
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-08-466-103A-14
; Sequence 14, Application US/08466103A
; Patent No. 5856124
; GENERAL INFORMATION:
; APPLICANT: Reppert, Steven M.
APPLICANT: Expert, Takashi
; TITLE OF INVENTION: HIGH-AFFINITY M
; TITLE OF INVENTION: RECEPTORS AND I
NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
                                         INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 23.2%
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           617/542-8906
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COMPUTER READABLE FORM:
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TYPE: PRT
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                                                                                                         63 LLFVTLLWIIELNVNGGIENTLEKEVMQYD--YYSSYFDIFLLAVFRFKVLILAYAVCRL 120
                                                                                                                                                                     121 RHWWAIALTTAVTSAFILLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
                                                                                                                                                                                         44;
                                                                            44;
                                                                                                                                                                                                                                                                                                                                 Query Match 6.4%; Score 77; DB 3; Length 353; Best Local Similarity 22.1%; Pred. No. 2.6; Matches 29; Conservative 20; Mismatches 38; Indels
                                             DB 2; Length 353;
                                                                           38; Indels
                                                                                                                                         148 LCYVFLIWMLTLI ---AİMPNLQTGTLQYDPRIYSCTF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows55
SOFTWARE: FastESG for Windows Version 2.0
UNRRENT APPLICATION DATA: US/09/280,420
                                           6.4%; Score 77; DB 2
22.1%; Pred. No. 2.6;
tive 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: 60/022,185
FILING DATE: 18-UUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/895,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0078(
TELECOMMUNICATION : FELECOMMUNICATION : 617/542-507
TELEPHONE: 617/542-890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ 1D NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acids
                                                            Best Local Similarity 22.18
Matches 29, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                      181 EEENRLLIVQD 191
                                                                                                                                                                                                                                                                      226 PDNKPKĽKPÓĎ 236
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FRAGMENT TYPE: internal
FRAGMENT TYPE: internal
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02110-2804
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   ; FRAGMENT 11F1
US-08-466-103A-14
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                                              Query Match
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US-09-479-195-2

US-09-479-195-2

US-09-479-195-2

Sequence 2, Application US/09479195

Patent No. 6326526

GENERAL INFORMATION:

APPLICANT: Reppert, Steven M.

APPLICANT: Reppert, Steven M.

TITLE OF INVENTION: MELATONIN RECEPTOR-DEFICIENT MICE AND USES THEREOF

FILE REPERENCE: 1021/72700

CURRENT APPLICATION NUMBER: US/09/479,195

CURRENT FILING DATE: 2000-01-07

PRIOR PILING DATE: 1998-07-24

PRIOR FILING DATE: 1998-07-24

PRIOR FILING DATE: 1998-07-24

PRIOR FILING DATE: 1998-07-24

SOFTWARE: PRESCO ID NOS: 12

SOFTWARE: PRESCO FOR Windows Version 3.0

SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 LLFVTLLWIIELNVNGGIENTLEKEVMQYD--YYSSYFDIFLLAVFRFKVLILAYAVCRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 RHWWAIALTTAVTSAFILLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 RHWWAIALTTAVTSAFILLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
                                                                         44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.4%; Score 77; DB 3
22.1%; Pred. No. 2.6;
tive 20; Mismatches
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Matches 29; Conservative
                                                                                                                                                                                             226 PDNKPKĽKPOD 236
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                                                                                                                                             181 EEENRLLIVQD 191
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US-09-479-195-2
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Length 234;
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Human angiogenesis related protein PRO1864 SEQ ID NO: 62.
WO200208284-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU89859 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU87980 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003032127-A1.
13-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1195; DB 5; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1195; DB 6;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003027278-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR65559 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003036159-A1.
20-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1195; DB 6;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU99499 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003040070-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted/transmembrane protein (PRO) #33. US2003032112-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 234 AA
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100.0%;
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100.0%;
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US2003027272-A1.
                                                                                                                                                                      GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                GERBER H.
GERRITSEN M E.
                                                                                                                                                                                                                                          (PANJ/) PAN J.
(PAON/) PAONI N F.
(STEB/) STEBHAN J F.
(WATA/) WATANABE C K.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                                                            GENENTECH INC
                                                                         BAKER K P.
FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 7
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Best Local Similarity
RESULT 12
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RESULT 10
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Best'Local Similarity
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU84295 standard;
                                                                                                                                                   GODDARD A.
                                      31-JAN-2002.
(GETH ) GENEJ
(BAKE/) BAKE
(FERR/) FERR
(GERB/) GERB
(GERR/) GERB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-FEB-2003.
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 GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 24, 2005, 16:12:47, Search time 157 Seconds
(without alignments)
534.667 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                       1: genescap1980s:*
2: genescap1990s:*
3: genescap2001s:*
4: genescap2001s:*
5: genescap2003s:*
7: genescap2003s:*
8: genescap2004s:*
8: genescap2004s:*
and is derived by analysis of the total score distribution.
                                                                                                                                  1 MNHLPEDMENALTGSQSSHA......EAGSEEAEEKQDSEKPLLEL 234
BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          query Match 100.0%; Score 1195; DB 4; Length 234; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1195; DB 4; Length 234; 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                               Searched:

Searched:

200273 segs, 358729299 residues
200273 segs, 358729299 residues
200274 segs, 358729299 residues
200274 segs, 358729299 residues
Maximum DB seg length: 200000000
Post-processing: Minimum Macch 100%
Listing first 1500 summaries
Database:

A Geneseg 235ep04:*
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US2002119130-Al.
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Human PRO1864 protein sequence SEQ ID NO:62.
WO200200690-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU29056 standard; protein; 234 AA.
Human PRO polypeptide sequence #33.
WO200168848-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM39929 standard; protein; 234 AA.
Human polypeptide SEQ ID NO 3074.
WO200153312-A1.
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                                                                                                 US-10-063-518-14
1195
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-2002.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(HYSE-) HYSEQ INC.
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WO200116318-A2.
                                                                                                                                  Sequence:
Scoring table:
                                                                                                                      Perfect score:
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Length 234;

Length 234;

Length 234;

us-10-063-518-14.rag.spdi

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Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
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                                                       ABU01691 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003027277-A1.
06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 20-FEB-2003.
PA (CETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 29
Score 1195; DB 6;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003040063-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human secreted polypeptide PRO1864, SEQ ID NO:66. US2003040064-Al.
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Pred. No. 1.3e-131;
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Human secreted/transmembrane protein (PRO) #33.
                                                                                                                                                                                                                                                                                                                                            #33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO33941 standard; protein; 234 AA.
Human secreted/transmembrane protein PRO1864
US2003009013-A1.
                                                                                                                                                                                                                                                                                                                          ABU86225 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO)
US2003036146-A1.
                                                                                                                                                                                        ABU89384 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003036141-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU80466 standard; protein; 234 AA.
Human PRO protein #33.
US2003036137-A1.
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23.JAN-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 32
   Query Match
Best Local Similarity
RESULT 25
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Best Local Similarity
RESULT 27
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Best Local Similarity
RESULT 28
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Best Local Similarity
RESULT 30
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Best Local Similarity
RESULT 31
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                                                                                                                                               Best Local Similarity RESULT 26
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                                                                                                                                     Query Match
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Novel human secreted and transmembrane protein PRO1864.
US2003017544-A1.
23-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU98770 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003013133-A1.
16-JAN-2003.
                                                                                                                                                                                                                              ABU96161 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
V02003036144-A1.
20-FEB-20034.
                                           100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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                                                                        Human secreted polypeptide PRO1864, SEQ ID NO:66. US2003027264-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARR94637 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003044926-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR74875 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003040056-A1.
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Human secreted/transmembrane protein (PRO) #33.
US2003040062-A1.
                                                                                                                                                                                                                                                                                                                                                         ABU92592 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003036149-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABO08669 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003044923-A1.
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US2003036140-A1.
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(GETH ) GENENTECH INC.
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Best Local Similarity
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Best Local Similarity
RESULT 17
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Best Local Similarity
RESULT 20
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     US2003036147-A1.
20-FEB-2003.
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Query Match
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RESULT 18

RESULT 19

Length 234;

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ABO06181 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003022294-A1.
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                                  100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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20 PEB-2003.
(GETH ) GENENTECH INC.
(GETY MATCh 100.0%; Score 1195; DB 6;
(ery Match 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                  Score 1195; DB 6;
Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted/transmembrane protein (PRO) #33.
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US2003044916-A1.
06-MAR-2003.
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Human secreted/transmembrane protein (PRO) #33.
05-P08-2003.
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Human secreted/transmembrane protein (PRO) #33.
US2003040060-A1.
                                                                                                          Human secreted/transmembrane protein (PRO) US2003036134-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU71512 standard; protein; 234 AA.
Human secreted polypeptide PRO1864.
US2003013855-A1.
16-JAN-2003.
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Best Local Similarity
RESULT 48
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Best Local Similarity
SSULT 54
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RESULT 45
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Best Local Similarity
RESULT 46
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Best Local Similarity
RESULT 50
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Best Local Similarity
RESULT 52
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                                                                                          ABU83380 standard;
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US2003036133-A1.
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Novel human secreted and transmembrane protein PRO1864.
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Novel human secreted and transmembrane protein PRO1864
US2003018183-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003032114-A1.
13-FEB-2003.
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Novel human secreted and transmembrane protein PRO1864
US2003032101-A1.
13-FEB-2003.
                                    100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003054474-A1.
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(ORIG-) ORIGENE TECHNOLOGIES INC.
100.0%; Score 1195; DB 6;
erry Match
100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                        ABR92197 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003036160-A1.
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Human secreted/transmembrane protein (PRO) #33.
US2003040054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABO11466 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003036124-A1.
20-FBB-2003.
                                                                                                                                                                                                                                        Human secreted/transmembrane protein (PRO) #33 US2003044925-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate selective polypeptide Pr340.
#V20003014298-A2.
                                                                                                                                                                                                                        ABO18838 standard; protein; 234 AA
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100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                  Query Match
Best Local Similarity
RESULT 35
ID ABR92197 standard; p
DE Human secreted polyp
PN US2003036160-A1.
PD 20-FEB-2003.
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Best Local Similarity
RESULT 37
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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US2003027267-A1.
                 06-FEB-2003.
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RESULT 39

Length 234;

Length 234;

Length 234;

Length 234;

Length 234;

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Query Match

Length 234;

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100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
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(GETH) GENENTECH INC.
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(GETH ) GENENTECH INC.
(GETY Match 100.0%; Score 1195; DB 6; Jery Match 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003027268-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1195; DB 6;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66
                                                                                                                                                                                                                                                                                                                                                                        ABR69328 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US20010361122-A1.
20-FEB-2003.
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003032137-Al.
13-FEB-2003.
                                                                                                                                              100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB001469 standard; protein; 234 AA. Human PRO polypeptide #33. US2003008353-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU81271 standard; protein; 234 AA. Human PRO polypeptide #33.
US2003017542-A1.
                                                               ABO07754 standard; protein; 234 AA. Human PRO polypeptide #33.
US2003032130-A1.
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(ORIG-) ORIGENE TECHNOLOGIES INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 72
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Best Local Similarity
RESULT 71
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Best Local Similarity
RESULT 68
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RESULT 69
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                     Best Local Similarity RESULT 65
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Novel human secreted and transmembrane protein PRO1864
US2003030117-A1.
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                               100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003027266-Al.
06-FEB-2003.
                                                                        RESULT 55
ID ABU65601 standard; protein; 234 AA.
E Human secreted/transmembrane protein, SEQ ID 66.
PN US2003036156-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABO15687 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003054483-A1.
                                                                                                                                                                                                                                                                                                                                                                               ABO03636 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33
US2003036128-A1.
O-FEB-2003.
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Human secreted/transmembrane protein, PRO1864.
US2003022298-A1.
                                                                                                                                                                                                                        ID ABO07449 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032117-Al.
PD 13-FEB-2003.
Ouery Match
Best Local Similarity 100.0%; Pred.
RESULT 57
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Human PRO polypeptide #33.
US22003032102-A1.
13-FEB-2003.
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Human PRO polypeptide #7.
US2002182638-A1.
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US2003036143-A1.
20-FEB-2003.
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(GETH ) GENENTECH INC.
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            (GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 56
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Best Local Similarity
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Best Local S
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RESULT 61
ID ABU72
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Novel human secreted and transmembrane protein PRO1864
US2003022300-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU82202 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003036136-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                        Human secreted polypeptide PRO1864, SEQ ID NO:66. US2003027271-Al.
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2002040068-A1.
                                                ABO27287 standard; protein; 234 AA.
Human secreted/transmembrane polypeptide PRO1864
US2003009012-A1.
(99-JAM-2003.
(GETH ) GENENTECH INC.
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Pred. No. 1.3e-131;
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Human secreted/transmembrane protein (PRO) #33.

20.FEB-2003.
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Human secreted/transmembrane protein (PRO) #33.
US2003032109-A1.
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US2003027280-Al.
06-FEB-2003.
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Query Match
Best Local Similarity
RESULT 85
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Best Local Similarity
RESULT 89
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RESULT 88
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RESULT 90
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Best Local Similarity
RESULT 91
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RESULT 94
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                  100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                         100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU90479 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003032108-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU93641 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003032119-A1.
                                                                                                                                                                                                                                                                           vuery Match
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 77
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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                                              Human secreted polypeptide PRO1864, SEQ ID NO:66. US2003027274-Al.
                                                                                                                                                                                           ABR71825 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US20032135-A1.
13-FEB-2003.
(GETH ) GENENTECH INC.
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Human secreted polypeptide PRO1864, SEQ ID NO:66
US2003027263-A1.
06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU88995 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US20030222297-A1.
30-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU83075 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003032105-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU83990 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003032111-A1.
                                                                                                                                                                                                                                                                                                                                      ABU85305 standard; protein; 234 AA. Human PRO polypeptide #33. US2003022295-A1.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 76
            Query Match
Best Local Similarity
RESULT 75
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Best Local Similarity
RESULT 78
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Best Local Similarity
SSULT 79
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06-FEB-2003
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Query Match

Query Match

RESULT 80
ID ABU94
DE Novel
PN US200
PD 13-FE

Query Match

Query Match Best Local &

RESULT 83

Query Match

100.0%; Pred. No. 1.3e-131;

Best Local Similarity

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Obstruction 100.0%; Score 1195; DB 6; Length 234;
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(GETH ) GENENTECH INC.
ery Match 100.0%; Score 1195; DB 6; Length 234;
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US2003032104-A1.
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Novel human secreted and transmembrane protein PRO1864.
US2003036155-A1.
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Novel human secreted and transmembrane protein PRO1864.
US2003022296-A1.
30-JAN-2003.
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US2003036157-A1.
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Novel human secreted and transmembrane protein PRO1864
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003027281-A1.
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003040058-A1.
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003032120-A1.
13-FEB-2003.
                                                                   Human secreted/transmembrane protein PRO1864.
US2003045684-Al.
USABR-2003.
(GETH ) GENENTECH INC.
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Human secreted polypeptide PRO1864.
US2003027212-A1.
                                 ABU92482 standard; protein; 234 AA.
                                                                                                                                                                                                                                                                                                                              ABU81770 standard; protein; 234 AA
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(GETH ) GENENTECH INC.
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LEB-2003.

LY Match
Best Local Similarity RESULT 104
ID ABO52267 stand<sup>c</sup>
DB Novel humar
PN US2003<sup>c</sup>
PD 06<sup>c</sup>
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Best Local Similarity
RESULT 101
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RESULT SID ABI DE HUI DE HUI DS US; PD 06- P
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Length 234;
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                                                                                                                                                                                                                                                                                                                                                         ABU86835 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003032131-A1.
13-FEB-2003.
                                                                   100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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(GETH ) 100.0$; Score 1195; DB 6;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003027262-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR70300 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003032139-A1.
13-PEB-2003.
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003036165-A1.
                                                                                                                                                                                                                                      ABU86530 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003032129-A1.
                                                                                                        Human PRO polypeptide #33. US2003032106-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU98465 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003022301-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 109

ID ABU94624 standard; protein; 234 AA.
DE Human PRO Polypeptide #33.
PN US2003032103-A1.
PD 13-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO04551 standard, protein, 234 AA.
Human PRO polypeptide #33.
US2003032107-A1.
13-FEB-2003.
ABU94319 standard, protein, 234 AA. Human PRO polypeptide #33. US2003017540-A1.
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Best Local Similarity
RESULT 115
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RESULT 110
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Best Local Similarity
RESULT 107
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RESULT 106
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                                                   23-JAN-2003.
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Length 234; Length 234; Length 234; Length 234; Length 234; 100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131; Length 234; Length 234; Length 234; Length 234; ABU90169 standard; protein; 234 AA. Novel human secreted and transmembrane protein PRO1864. US2003036153-A1. ABU98269 standard; protein; 234 AA. Novel human secreted and transmembrane protein PRO1864. US2002183493-A1. ABU91076 standard; protein; 234 AA. Novel human secreted and transmembrane protein PRO1864 US2003036154-A1. 20-PEB-2003. 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131; 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131; 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131; 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131; 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131; 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131; Query Match 100.0%; Score 1195; DB 6; Best Local Similarity 100.0%; Pred. No. 1.3e-131; 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131; 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131; ABR70910 standard; protein; 234 AA. Human secreted polypeptide PR01864, SEQ ID NO:66. US2003040069-A1. ABU92897 standard; protein; 234 AA. Human secreted/transmembrane protein (PRO) #33. US2003036142-A1. AB009584 standard; protein; 234 AA. Human secreted/transmembrane protein (PRO) #33. US2003044931-A1. ABO10856 standard; protein; 234 AA. Human secreted/transmembrane protein (PRO) #33. US2003036150-A1. Human PRO polypeptide #33.
0S2003022593-A1. ABU91386 standard; protein; 234 AA. Human PRO polypeptide #33. ABU79506 standard; protein; 234 AA. Human PRO polypeptide #33. US2003032110-A1. ABU95856 standard; protein; 234 AA. Human PRO polypeptide #33. US2003036145-Al. 20-FEB-2003. 05-DEC-2002. (GETH ) GENENTECH INC. Query Match Best Local Similarity RESULT 123 Query Match Best Local Similarity RESULT 122 Query Match Best Local Similarity RESULT 118 Best Local Similarity RESULT 119 Local Similarity Query Match Best Local Similarity 20-FEB-2003. 06-MAR-2003. 20-PEB-2003. 20-FEB-2003. 13-FEB-2003. 27-FEB-2003. 30-JAN-2003 Query Match Query Match RESULT 120
ID ABO095
DE Human
PN US2003
PD 06-MAR RESULT 124

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Length 234;
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Novel human secreted and transmembrane protein PRO1864.
                                                                                           Novel human secreted and transmembrane protein PRO1864 US2003036634-A1.
                            100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Préd. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003032122-A1.
                                                                                                                                                                                                          ABU84600 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003032116-A1.
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Human secreted/transmembrane protein (PRO) #33.
US2003036152-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABO09889 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003017543-A1.
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US2003036139-A1.
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US2003027993-A1.
                                                                               protein; 234 AA
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06-FEB-2003.
(GETH ) GENENTECH INC.
100.0%;
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RESULT 127
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PA (GETH) GENENTECH INC.

Query Match 100.0%;

Best Local Similarity 100.0%;
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Human PRO polypeptide #33.
US2003017541-Al.
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(GETH ) GENENTECH INC.
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RESULT 135
                              Query Match
Best Local Similarity
RESULT 126
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Best Local Similarity
RESULT 128
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Best Local Similarity
RESULT 129
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Best Local Similarity
RESULT 132
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Best Local Similarity
RESULT 133
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                                                                            ABU89274 standard;
US2003032128-A1.
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ABR80849 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003049741-A1.
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Abovel human secreted and transmembrane protein PRO1864.
US2003008352-Al.
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ID ABU96760 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864
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(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

100.0$; Score 1195; DB 6;

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100.0$; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003054455-A1.
                                                           Query Match 100.0%; Score 1195; DB 6; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 136
                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003040076-A1.
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Human secreted(transmembrane protein (PRO) #33.
US2003032118-A1.
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Human secreted/transmembrane protein (PRO)
US2003044922-A1.
06-MAR-2003.
                                                                                                                  ABU72115 standard; protein; 234 AA.
Human PRO polypeptide #7.
US2003023042-A1.
                                                                                                                                                                                                                                                                protein; 234 AA
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Human PRO polypeptide #33.
US2003032115-A1.
13-FEB-2003.
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(GETH ) GENENTECH INC.
                                     12-SEP-2002.
(GETH ) GENENTECH INC.
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RESULT 142
ID ABO05571 standard; pr
DE Human secreted/transm
PN US2003032118-A1.
PD 13-FEB-2003.
                                                                                                                                                                            30-JAN-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 143
ID ABR71960 standard; p)
B Human secreted polype
PN US2003036135-A1.
PD 20-FEB-2003.
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Best Local Similarity
REGULT 139
ID ABR70605 standard; px
DE Human secreted polype
pn US20030400076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 145
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Best Local Similarity
RESULT 144
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Best Local Similarity
RESULT 137
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Best Local Similarity
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Best Local Similarity
                  US2002127584-A1.
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Query Match 100.0%; Score 1195; DB 6; Length 234; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 154
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Human secreted/transmembrane protein (PRO) #33.

PN US20030686885-A1.

PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 151
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(GETH ) GENENTECH INC.
100.0%; SCORE 1195; DB 6;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068752-A1.
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13-MRAE-2003.
(GETH ) GENENTECH INC.
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100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003049769-A1.
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003054479-A1.
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068743-A1.
                                                                                     ABR81154 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003049743-A1.
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Human Secreted/transmembrane protein (PRO) #33.
US2003068725-A1.
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Human secreted/transmembrane protein (PRO) #33
US2003068682-A1.
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RESULT 153
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
13-MAR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 149
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RESULT 150
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Best Local Similarity
RESULT 147
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RESULT 152
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Pred. No. 1.3e-131;

#33.

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Best Local Similarity 100.0%; Pred. No. 1.3
RESULT 164
ID ABO21485 standard; protein; 234 AA.
DB Human secreted/transmembrane protein (PRO)
PN US2003054471-A1.
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(GETH ) GENENTECH INC.
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Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM24758 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003104539-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR90282 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003040075-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABM17196 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003054459-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR94942 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003044930-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR95247 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003040071-A1.
                                                                                                                                                                                                                                                                                  ADA77818 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003073180-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO03026 standard; protein; 234 AA. Human secreted/transmembrane protein (PRO) #33 US2003036131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB17071 standard; protein; 234 AA.
Human transmembrane PRO polypeptide (SeqID 14)
US2003050462-A1.
                                                                                                                             ABO43963 standard; protein; 234 AA. Human PRO polypeptide #33. US2003068755-A1. 10-APR-2003. (GETH ) GENENTECH INC.
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 Human PRO polypeptide #33. US2003068701-A1.
                                                                                                                                                                                                                                                                                                                                           17-APR-2003.
(GETH ) GENENTECH INC.
                                         10-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
RESULT 158
ID AB003026 standard; pi
DE Human secreted/transn
PN US2003036131-A1.
PD 20-FEB-2003.
                                                                                                                                                                                                                                           Best Local Similarity RESULT 156
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RESULT 162
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ID ABO439
DE Human
PN US2003
PD 10-APR
PA (GETH
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Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
                                     Length 234;
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                                   Score 1195; DB 6;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                    Query Match 100.0%; Score 1195; DB 6; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1195; DB 6;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABM36283 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2001104549-A1.
05-JUN-2003.
(GETH ) GENENTECH INC.
ery Match
100.0$; Score 1195; DB 6;
st Local Similarity 100.0$; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                 HAW77578 standard; protein; 234 AA.

Human secreted polypeptide PRO1864, SEQ ID NO:66.
US200305473-A1.
20-MAR-2003.
(GEH) GENENTECH INC.
ery Match
st Local Similarity 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Auman secreted polypeptide PRO1864, SEQ ID NO:66. US2002073183-A1.
                                                                                             ABR97749 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064452-A1.
                                                                                                                                                                                                                                                        ABR87537 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068705-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM27808 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064440-A1.
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM01595 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068722-A1.
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PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195;

Best Local Similarity 100.0%; Pred. No. 1.3

RESULT 171

ID ABM35046 standard; protein; 234 AA.
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17-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%;

Best Local Similarity 100.0%;
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PA (GETH ) GENENTECH INC.

QUETY MATCh

Best Local Similarity 100.0%;

RESULT 167
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PA (GETH ) GENENTECH INC.

QUETY MATCh

Best Local Similarity 100.0%;

RESULT 170
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 169
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
                        US2003068707-A1.
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068699-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM29028 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068721-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABM15976 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064463-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1195; DB 6;
Pred. No. 1.3e-131
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A (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
                                                                                              Score 1195; DB 6;
Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064447-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABMO2680 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003073184-A1.
                                                                                                                                                   ABRÍ2807 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064462-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO27537 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003064451-A1.
                                                                                                                                                                                                                                                                                       ABO24568 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003065159-A1.
                              Human secreted/transmembrane protein (PRO) #33.
US2003049749-A1.
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                 ABO48065 standard; protein; 234 AA.
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10-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                   (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 180
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Best Local Similarity
RESULT 178
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RESULT 181
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Best Local Similarity
RESULT 182
ID ABM21098 standard;
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                                                                                                                   Local Similarity
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Best Local Si
RESULT 175
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RESULT 177
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Length 234;
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 184
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                                            Length 234;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN76054 standard; protein; 234 AA.

ALMAIN secreted polypeptide PRO1864, SEQ ID NO:66.
US203104548-A1.
05-JUN-2003.
(GETH) GENENTECH INC.
(GETH) 100.08; Score 1195; DB 6; eLy Match
St. Local Similarity 100.08; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM25673 standard; protein; 234 AA. Human secreted polypeptide PRO1864, SEQ ID NO:66.US2003104542-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABM25978 standard; protein; 234 AA. Human secreted polypeptide PRO1864, SEQ ID NO:66. US2003104543-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                               100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN76358 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003082717-A1.
01-MAY-2003.
                                                                                                  ABM09444 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003073175-A1.
                                              Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D ABO03331 standard; protein; 234 AA.

E Human secreted/transmembrane protein (PRO) #33.

N US2003036127-A1.

D 20-FBB-2003.

Query Match
                                                                                                                                                                                                                                        ABO41314 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003068695-A1.
                                                                                                                                                                                                                                                                                                                                                                          Human PRO polypeptide #33.
US2003068703-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO43658 standard; protein; 234 AA. Human PRO polypeptide #33.
US2003068732-Al.
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%;
RESULT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 186
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Best Local Similarity
RESULT 191
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Best Local Similarity
RESULT 190
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Best Local Similarity
RESULT 185
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Length 234;

Length 234;

Length 234;

Length 234;

us-10-063-518-14.rag.spdi

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PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USANCE OF THE NO. 100.0%; Score 1195; DB 6; lery Match 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 03-APR-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 205
                                                                                                                                                                                          PD 10-APR-2003.

PA (GETH ) GENENTECH INC.

QUECY Match 100.0%; Score 1195; DB 6;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1195; DB 6;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                        ABR87842 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068718-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABMO8834 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM04874 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068727-A1.
                                                                                                                                                                                                                                                                                                   ABO27842 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003064454-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB029977 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003064461-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO39484 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
10-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO36434 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003068714-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB035519 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003068758-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003uoo...
10-APR-2003.
(GETH ) GENENTECH INC,
100.0%;
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PA (GETH) GENENTECH INC.

Query Match 100.0%;

Best Local Similarity 100.0%;

RESULT 204
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Best Local Similarity 100.0%;
RESULT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO33186 standard, proteir
Human PRO polypeptide #33.
US2003068724-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 208
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RESULT 206
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SULT 210
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                                                                                                                                                                                                                                                                                                                              Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1195; DB 6; Length 234; Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                   Length 234;
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Local Similarity 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 234;
                                                                                                                                                                                                            ABO44245 standard; protein; 234 AA.
Human secreted/transmembrane polypeptide PRO 1864.
US2003018172-A1.
               100.0%; Pred. No. 1.3e-131;
                                                                                                                                               100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                         100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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BESULT 200

B ABR93112 standard; protein; 234 AA.

B Human secreted polypeptide PR01864, SEQ ID NO:66.

PN US2003064465-A1.

PD 03-APR-2003.

PA (GETH) GENENTRUT TNO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 1195; DB 6; Local Similarity 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                              ABR90587 standard, protein, 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003036130-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR73655 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003054468-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR94332 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
06-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 198

ID ABR75839 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US2003044929-A1.

PD 06-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR93417 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003054478-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abolé907 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003054470-A1.
                                                        ABO02416 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33
US2003040061-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                23-JAN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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               Best Local Similarity
                                                                                                                                                                   Local Similarity
                                                                                                                               27-FEB-2003.
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Length 234;

Length 234;

Length 234;

Length 234;

Length 234;

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13-MAR-2003.
(GETH ) GENENTECH INC.
100.0%; Score 1195; DB 6; Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                             Length 234;
          Length 234;
                                                                                                                                           Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JF 215
ADA19876 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003069394-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR97139 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003054481-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR86927 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003049778-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1195; DB 6;
Pred. No. 1.3e-131;
        Query Match 100.0%; Score 1195; DB 6; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 211
                                                                                                                                           100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                           ABMI1884 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003104555-A1.
05-UNA-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                           100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                         ABMI0359 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003069407-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB17259 standard; protein; 234 AA.
Human transmembrane PRO polypeptide (SeqID 14).
US2003050465-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO23653 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003032134-A1.
                                                                                                                                                                                                                                                                                                                       ABO52030 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003049768-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO52335 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003049771-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US200303.
20-MAR-2003.
(GETH ) GENENTECH INC.
100.0%;
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10-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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Local Similarity 1
RESULT 216
ID ABO23653 stand-
DE Human ser
PN US200
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                10-APR-2003.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
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                                                                                                                                            Query Match
Best Local Similarity
RESULT 212
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 217
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RESULT 214
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Score 1195; DB 6; Length 234; Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 234;
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                                                                                                                                               Length 234;
                                                                                                                                                                                                                                                                                                                100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
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PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 1195; DB 6; Best Local Similarity 100.0%; Pred; No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM22318 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068740-A1.
10-APR-2003.
GETH ) GENENTECH INC.
ery Match
set y Match
set inilarity 100.0%; Score 1195; DB 6; Score Similarity 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068716-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM07614 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66
US2003068751-A1.
Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM06394 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068709-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted polypeptide PRO1864, SEQ ID NO:66 US2003068692-A1.
                                             ABMI0969 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003049782-A1.
                                                                                                                                                    100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                 ABM28113 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003054476-A1.
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                                                                                                                                                                                                                                                                                                                                                                           ABO32112 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003068733-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted/transmembrane protein (PRO)
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ID ABO40704 standard; protein; 234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM15239 standard; protein; 234 AA
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10-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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(GETH) GENENTECH INC.

Query Match 100.0%;

Best Local Similarity 100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                            13-MAR-2003.
(GETH ) GENENTECH INC
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RESULT 226
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Best Local Similarity
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Best Local Similarity
RESULT 224
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(GETH ) GENENTECH INC.

100.0%; Score 1195; DB 6;

100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                  Score 1195; DB 6;
Pred. No. 1.3e-131;
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PA (GETH ) GENENTECH INC.

QUENTY MATCh

100.0%; Score 1195; DB 6;

Best Local Similarity 100.0%; Pred. No. 1.38-131;

RESULT 242
                                                                                   ABM01155 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003049770-A1.
                                                                                                                                                                                                                                                                                                                   Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                        ABM13409 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064457-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted polypeptide PRO1864, SEQ ID NO:66. US2002068711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1195; DB 6;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003067478-A1.
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003073185-A1.
                                                                                                                                                                                                                                       ABR88757 standard; protein; 234 AA. Human secreted polypeptide PRO1864, SEQ ID NO:66. US2003073169-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted/transmembrane protein (PRO) #33.
US2003049745-A1.
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Human secreted/transmembrane protein (PRO) #33.
US2003049751-A1.
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, (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195;
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Human secreted/transmembrane protein (PRO)
US2003068773-A1.
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13-MAR-2003.
(GETH ) GENENTECH INC.
"arch 100.0%; SC
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13-MAR-2003.
(GETH ) GENENTECH INC.
100.0%;
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10-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                             Query Match
Best Local Similarity
RESULT 239
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Best Local Similarity
RESULT 243
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Best Local Similarity
RESULT 241
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Best Local Similarity
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                             ABM35351 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003073179-A1.
                                                                                                                          100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003054480-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR80544 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US203049940-A1.
13-MAR-2003.
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003059885-A1.
                                                                                                                                                                                ABM33114 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66
US2003087374-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU99194 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003040055-A1.
27-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABO50200 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003049777-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABO04246 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33
20-FBB-2003.
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Human secreted/transmembrane protein (PRO) #33.
US2003040074-A1.
                                                                                                                                                                                                                                                                                                                   ABO52640 standard; protein; 234 AA. Human PRO polypeptide #33.
US2003049773-A1.
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(GETH ) GENENTECH INC.
                                                                                                          (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 238
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Best Local Similarity
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           RESULT 229
ID ABM353
DE Human
PN US2003
PD 17-APR
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Length 234;

#33.

Length 234;

DB 6;

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GENENTECH INC.
                              Query Match
Best Local Similarity
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10-APR-2003
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064456-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003049772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM16586 standard; protein; 234 AA. Human secreted polypeptide PRO1864, SEQ ID NO:66. US2003064448-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003049758-A1.
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                  100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                ABR96224 standard; protein; 234 AA. Human secreted polypeptide PR01864, SEQ ID NO:66.US2003054458-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted polypeptide PRO1864, SEQ ID NO:66.
US203059886-A1.
      100.0%; Pred. No. 1.3e-131;
                                                                                                                                               ABM74834 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003096353-A1.
                                                      SEQ ID NO:66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO29062 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003068693-A1.
                                                                                                                                                                                                                                                                ADA79610 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003073173-A1.
                                     ABM22623 standard; protein; 234 AA. Human secreted polypeptide PRO1864, US2003087373-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM02375 standard; protein; 234 AA.
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03-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 254
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RESULT 257
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Best Local Similarity
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Best Local Similarity
RESULT 249
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Best Local Similarity
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Best Local Similarity
        Best Local Similarity
                                                                                            08-MAY-2003.
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Length 234;
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Length 234;
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1.3e-131;
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Pred. No. 1.3e-131;
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
EFY MATCh 100.0%; Score 1195; DB 6;
EFY MATCh 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003096339-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABM6367 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068737-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM75749 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003104547-A1.
   100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                      100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                        ABM22013 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068742-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM28418 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003082715-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM28723 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003082716-A1.
                                                                                                                                                                                                  ABM23233 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068753-A1.
                                              ABM23843 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068735-A1.
                                                                                                                                             100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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(GETH) GENENTECH INC.

Query Match 100.0%; Score 1195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB037654 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO)
US2003068756-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1195;
Pred. No. 1.
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05-UUN-2003.
(GETH ) GENENTECH INC.
100.0%;
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PA (GETH ) GENENTECH INC.

QUETY MATCH

Best Local Similarity 100.0%;

RESULT 265
                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                10-APR-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 266
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Best Local Similarity
RESULT 261
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Best Local Similarity
RESULT 263
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Length 234;
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(GETH ) GENENTECH INC.
100.0%; Score 1195; DB 6;
lery Match of milarity 100.0%; Pred. No. 1.3e-131;
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10-PR-2003.
10-TH ) GENENTECH INC.
100.0%; Score 1195; DB 6;
100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003073172-A1.
17-APR-2003.
                                                                                                                 Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                ABM00240 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003073172-A1.
17-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0%; Pred. No. 1.38-131; RESULT 279
ID ABM21538 standard; protein; 234 AA.
DB Human secreted polypeptide PRO1864, SEQ ID NO:66. PN US2003068736-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM20408 standard; protein; 234 AA. Human secreted polypeptide PRO1864, SEQ ID NO:66.052003104557-A1.05-UNA-2003.
                                                                                                                                                                                                                                                                                                                                                          Score 1195; DB 6;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted/transmembrane protein (PRO) #33. US2003068700-A1.
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Human secreted/transmembrane protein (PRO) #33.
US2003027276-A1.
06-FBB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO38264 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33
US2003068767-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABO45564 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003073182-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO29672 standard; protein; 234 AA.
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17-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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100.0%;
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RESULT 284
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 278
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RESULT 282
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Best Local Similarity
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Best Local Similarity
RESULT 277
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Query Match
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                                                        100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                     100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
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Best Local Similarity 100.0%; Score 1195; DB 6;
RESULT 292
ID ABR89672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003031317.A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1195; DB 6; Beet Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 290
                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM13714 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064458-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR92502 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003064446-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR81459 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003049744-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM77883 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003049783-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM26588 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003032121-Al.
13-FEB-2003.
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Human secreted/transmembrane protein (PRO) #33.
                                                                                                                   ABO18228 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
05-2003044920-A1.
06-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                  AB022960 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003054461-A1.
                                                                                                                                                                                                                                                           ABO22655 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003027265-A1.
06-FEB-2003.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Query Match 1
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(GETH ) GENENTECH INC.
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Lery Match
Best Local Similarity
RESULT 286
ID AB018228 star²
DE Human ser
PN US?"
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Best Local Similarity
RESULT 293
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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 298
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(GETH) GENENTECH INC.
ery Match 100.0%; Score 1195; DB 6; Length 234;
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                                                                           Score 1195; DB 6; Length 234; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                               ABM03000 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068734-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM25063 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2001304540-A1.
05-UM-2003.
                                                                                                                                                                                                                        Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                          ABM07309 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068702-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO47760 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
USC033049747-Al.
13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABO37044 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABO47455 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003049742-A1.
                                                                                                                                                Human secreted/transmembrane protein (PRO) #33 US2003064464-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO41619 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO)
US2003068729-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO35214 standard; protein; 234 AA
Human PRO polypeptide #33.
US2003068738-A1.
                                                                                                                                     protein; 234 AA
US2003064460-A1.
03-APR-2003.
(GETH ) GENENTECH INC.
"...ch 100.0%; SC/
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13-MAR-2003.
(GETH ) GENENTECH INC.
100.04;
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10-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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10-APR-2003.
(GETH ) GENENTECH INC.
(GETH) CALL 100.0%;
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PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%;
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 303
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Best Local Similarity
RESULT 301
                                                                                            Best Local Similarity RESULT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 300
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                                                                                                                                   ABO30282 standard;
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100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 306
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( GETH ) GENENTECH INC.

QUETY MATCH

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003040078-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003054462-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR79629 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003040059-A1.
27-FEB-2003.
                                                             .....s.v standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003049750-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABOSOSOS standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003049779-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABO20875 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003032132-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO17923 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003044918-A1.
                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO polypeptide #33.
US2003049767-A1.
                                                                                                                                                                                                                                          ABOS1420 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003049766-A1.
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Best Local Similarity 100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity 1
RESULT 309
ID ABR79629 standard; pro
DE Human secreted polypep
PN US2003040059-A1.
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                     Query Match
Best Local Similarity
RESULT 305
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Best Local Similarity
RESULT 314
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Best Local Similarity
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Best Local Similarity
RESULT 310
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Length 234;
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                                                                          (GETH) GENENTECH INC.

(GETH) GENENTECH 100.0%; Score 1195; DB 6;

iry Match

ir Local Similarity 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                      ABMI6281 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US20034449-A1.
03-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1195; DB 6;
Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003104541-A1.
ABM12189 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064445-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABM14629 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068696-A1.
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Pred. No. 1.3e-131;
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ID ABM09139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073174-A1.
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003104545-A1.
05-7UN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                               ABM24148 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064441-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM04510 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068712-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM06699 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABO39179 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003068775-A1.
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Best Local Similarity 100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                         Best Local Similarity
RESULT 315
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Best Local Similarity
RESULT 316
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                                                                   03-APR-20
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GENENTECH INC.
US2003054467-A1.
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(GETH ) GEN
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                     Length 234;
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(GETH ) GENENTECH INC.
(ery Match | 100.0%; Score 1195; DB 6;
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                     100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US203032136-Al.
13-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003036129-Al.
20-FEB-2003.
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Pred. No. 1.3e-131;
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003040057-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR73350 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66
                                                                                                                                                                                                                                                                                                                 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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                                                                          ABM19878 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003104554-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO06839 standard; protein; 234 AA. Human secreted/transmembrane protein (PRO) #33. US2003040053-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA83135 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003049752-A1.
                                                                                                                                                                                                                        ABO46784 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003049762-A1.
                                                                                                                                                                                                                                                                                                                                                                   ABO47089 standard, protein; 234 AA.
Human PRO polypeptide #33.
US2003049765-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                 13-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2003.
(GETH ) GENENTECH INC
                                                                                                                                                                               Best Local Similarity RESULT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 326
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Best Local Similarity
                                  Best Local Similarity RESULT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-2003.
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   05-JUN-2003.
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Best Local Si
RESULT 327
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PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 234;
100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                100.0%; Score 1195; DB 6; Length 234; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                       Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                 CG-WAR-2003.
(GETH) GENENTECH INC.
(GETH ) GENENTECH INC.

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(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1195; DB 6;
Pred. No. 1.3e-131;
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Pred; No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1195; DB 6; Best Local Similarity 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1195; DB 6;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR79934 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003049738-A1.
                                                                                                                                                                                                                                                                     100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR94027 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003059879-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM11274 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064469-A1.
                                        Human secreted polypeptide PRO1864, SEQ ID NO:66. US200322-A1.
                                                                                                                                                                                            ABR73045 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003027270-A1.
06-FBB-2003.
                                                                                                                                                                                                                                                                                                             Human secreted polypeptide PRO1864, SEQ ID NO:66. US200354469-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABO20570 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003032126-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO25313 standard; protein; 234 AA. Human PRO polypeptide #33.
US2003054463-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0%;
RESULT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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Best Local Similarity 100.0%;
RESULT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB025618 standard; protein;
Human PRO polypeptide #33.
US200305466-A1.
20-MAR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                    Est Local Similarity
RESULT 334
ID ABR76444 standard; g
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 337
                                                                                                                                                                                                                                                                                           Best Local Similarity
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Best Local Similarity
RESULT 338
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RESULT 340
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SULT 335
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Query Match
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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 347
                                                                                                                                                                                                                                                                                                Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1195; DB 6; Length 234; Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
                                                                                                                             Length 234;
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PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 351
                                                                                                                         100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                              100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 100.0%; Score 1195; DB 6; Local Similarity 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABMO5479 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003045700-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM15544 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068698-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM06529 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068759-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABM27198 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66
US2003068760-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABM29943 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US200368769-A1.
10-ARP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                    AB030587 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003064466-A1.
                                                                                                                                                                                                                                                                                                                                                           ABO30892 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33
US2003064468-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB042229 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33
US2003049748-A1.
                      ABO32881 standard; protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
RESULT 352
                                       Human PRO polypeptide #33.
US2003064453-A1.
03-APR-2003.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                      03-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 345
                                                                                                                                          Best Local Similarity RESULT 344
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                Query Match
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RESULT 343
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Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 234;
ID AB037959 standard; protein; 234 AA.

DE Human secreted/transmembrane protein (PRO) #33.

PN U22003068765-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Pred. No. 1.3e-131;

REGULT 353
                                                                                                                                                                                                                    13-MAR-2003.
(GETH ) GENENTECH INC.
ery Match 100.0%; Score 1195; DB 6;
ery Match 100.0%; Pred. No. 1.3e-131;
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
lery Match 100.0%; Score 1195; DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 360
                                                                                                                                                                                                                                                                                                                                                                                        PA (GETH ) GENENTECH INC.
Query Match
100.0%; Score 1195; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA00345 standard; protein; 234 AA.
Human secreted/transmembrane polypeptide PRO 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                      ABM66672 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068688-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABMI9573 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003104552-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR88147 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068720-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 358
ID ABO49590 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049775-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB20178 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003082767-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABO49285 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33
US2003049774-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA78430 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33
US2003073181-A1.
                                                                                                                                                          ABO45869 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003049754-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 10.APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%;
RESULT 361
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Best Local Similarity
RESULT 356
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Best Local Similarity
RESULT 357
                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 354
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RESULT 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U3-MAR-2003.
(GETH) GENENTECH INC.
ery Match 100.0%; Score 1195; DB 7; Length 234;
ery Match 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 234;
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                                               Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1195; DB 7;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 1195; DB 7; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR74570 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003044924-A1.
06-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM17806 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003040072-A1.
                                                                                                                                                                                100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                              100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR77049 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003044927-A1.
06-MAR-2003.
                                                 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.3e-131;
                                                                                                ABM26893 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068739-A1.
                                                                                                                                                                                                                              ABM01290 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO05266 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003036126-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABOSOB10 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003049780-A1.
                                                                                                                                                                                                                                                                                                                                                             ABO39789 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003068689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB049895 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33
US2003049776-A1.
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(GETH ) GENENTECH INC.
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Ludy Match
Best Local Similarity
RESULT 367
ID ABO05266 stand
DE Human ser
PN US20
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Leff-Al.
Leff-Al.
Leff-Al.
Best Local Similarity
RESULT 368
ID ABR74570 stand
DE Human ser
                                                                                                                                                                                                                                                                                   10-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
                                   (GETH ) GENENTECH INC.
                                                                                                                                                   10-APR-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 366
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                                                                  Local Similarity
   US2003027992-A1.
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Length 234;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068717-A1.
                                                                                                                                                                                                                            100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Best Local Similarity 100.0%; Score 1195; DB 7;
RESULT 376
DD ABM10664 standard; protein; 234 AA.
DE Human secreted polypeptide PR01864; SEQ ID NO:66.
PN US2003064455-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM76663 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003054465-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR89367 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003073170-A1.
17-ARR-2003.
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003073176-A1.
                                                                          100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR86012 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66
US2003049759-A1.
                     SEQ ID NO:66
                                                                                                                                                                                                                                                                                 ABO19960 standard; protein; 234 AA.
Human secreted(transmembrane protein (PRO) #33.
US2003032124-A1.
PFEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                 ABO24263 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003064467-A1.
                                                                                                                                ABO21790 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003054475-A1.
ABR95857 standard; protein; 234 AA.
Human secreted polypeptide PRO1864,
US2003046073-A1.
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20-MAR-2003.
(GETH ) GENENTECH INC.
100.0%;
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17-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 100.0%;

RESULT 377
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 375
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Best Local Similarity
RESULT 378
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Best Local Similarity
RESULT 379
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Best Local Similarity
RESULT 372
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Query Match
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RESULT 390
                                                                                                                                                                                       Length 234;
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Pred. No. 1.3e-131;
                                     Length 234;
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                                   Query Match 100.0%; Score 1195; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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ID ABM18963 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104550-A1.
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Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                          ABM02985 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US20031068764-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM19268 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003104551-A1.
05-UNA-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR89062 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003036119-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR72435 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003036120-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR69023 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66
US200327273-A1.
06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO48980 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003049757-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO46479 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003049761-AI.
                                                                                          ABO34909 standard; protein; 234 AA. Human PRO polypeptide #33. US2003068728-A1.
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100.0%;
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AH GENENTECH IN

LY MATCH

Best Local Similarity IN

RESULT 384

ID ABM19268 standa-

DE Human secre-

PN US20031
                                                                                                                                                 10-APR-2003.
(GETH ) GENENTECH INC.
                 (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC
                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 382
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10-APR-2003
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03-APR-2003.
(GETH) GENENTECH INC.
ery Match 100.0%; Score 1195; DB 7; Length 234;
                                                                                                              Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN U32003059882-A1.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 1195; DB 7; Ler

RESULT 394

ID ABM02070 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US200305984-A1.

PD 27-MAR.2003.

PA (GETH) GENENTECH INC.

Query Match

100.0%; Score 1195; DB 7; Ler

RESULT 395

RESULT 395
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Query Match
100.0%; Score 1195; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 393
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003036161-A1.
US2003036161-A1.
(GETH ) GENENTECH INC.
ery Match
st Local Similarity 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                           100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003073186-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1195; DB 7;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM30553 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064443-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 03-APR-2003.

PA (GETH ) GENENTECH INC.

QUERY MAtch 100.0%; Score 1195; DB 7;

Best Local Similarity 100.0%; Pred. No. 1.38-131;

RESULF 398
                                                                                                                                                                                                                                                                                                                       ABR80239 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003049739-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM24453 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064444-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR87232 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068687-A1.
                                                                                                                                                                     ABO18533 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003044921-A1.
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17-APR-2003.
(GETH ) GENENTECH INC.
"arch 100.0%; SC
                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 392
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Best Local Similarity
RESULT 397
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Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 409
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                                                                                                 Length 234;
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(GETH ) GENENTECH INC.
ary Match 100.0%; Score 1195; DB 7;
ary Match 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003040067-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003104538-A1.
05-UNA-2003.
                                                                                                   100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                             100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABM09749 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003073178-A1.
                                                                                                                                                                                                                                                                                               ABMI4324 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66
US2003068686-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABOS1115 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003049781-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABO03941 standard; protein; 234 AA.
Human secreted(transmembrane protein (PRO) #33.
US2003036158-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABO38874 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003068774-A1.
                                                                                                                                                       ABO31197 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003208710-A1.
(GETH ) GENENTECH INC.
                            Human secreted/transmembrane protein (PRO) #33.
US2003068697-A1.
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100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
                                                                   10-APR-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 404
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RESULT 403
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Length 234;
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
100.0%; Score 1195; DB 7;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064442-Al.
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003064450-A1.
                                                                          100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003073177-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                       ABM01765 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66
US2003059883-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM78188 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003049764-A1.
                                                                                                                                                                                                                                                                              ABR93722 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003054457-A1.
20-MAR-2003.
ABR78864 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003054456-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABO31807 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003068731-A1.
                                                                                                                               ABO22958 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003205482-A1.
(GETH ) GENENTECH INC.
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03-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 100.0%;

RESULT 414
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PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 100.0%;

RESULT 415
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 413
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RESULT 417
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RESULT 412
                                                                              Query Match
Best Local Similarity
RESULT 410
                                                              20-MAR-2003.
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100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
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10-APR-2003.
(GETH ) GENENTECH INC.
100.0%; SC
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Best Local Similarity 100.0%;
RESULT 435
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PA (GETH) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%;
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Best Local Similarity 100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 431
     Query Match
Best Local Similarity
RESULT 428
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Best Local Similarity
RESULT 430
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RESULT 437
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Best Local Similarity
RESULT 429
                                                                                                                    06-MAR-2003.
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(GETH ) GENENTECH INC.
ery Match 100.0%; Score 1195; DB 7; Length 234;
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(GETH ) GENENTECH INC.
(EFY Match 100.0%; Score 1195; DB 7;
(ery Match 100.0%; Pred. No. 1.3e-131;
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ABM14019 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068683-A1.
10-APR-2003.
                                                                                 100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                    ABM08224 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003068754-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                             ABM74529 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003096351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM33724 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003096358-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM20183 standard; protein; 234 AA.
Human secreted polypeptide PR01864, SEQ ID NO:66.
US2003104556-A1.
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003036122-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR85097 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US203040065-A1.
27-FEB-2003.
                                                                                                                                                                                                                                                                                             ABO40094 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
10-APR-2003.
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Human secreted/transmembrane protein (PRO) #33.
US2003049756-A1.
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Human secreted/transmembrane protein (PRO) #33
US2003036121-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
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ID ABM745
DE Human
PN US2003
PD 22-MAY
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Length 234;
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Pred. No. 1.3e-131;
                                                                                                     Score 1195; DB 7;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABM76968 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003054464-A1.
20-MRA-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR85402 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003049746-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM22928 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068757-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM30248 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068723-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1195; DB 7;
Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068741-A1.
                                                                                                                                                                                                                                                                                                                                                ABMI7501 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003044928-A1.
ABO15077 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003044919-A1.
                                                                                                                                                                           ABO17212 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #333
US2003040077-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO28147 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003064459-A1.
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US2003049735-A1.
                                    (GETH )
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(GETH ) GENENTECH INC.
ery Match
ery Match 100.0%; Score 1195; DB 7; Length 234;
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Novel human secreted and transmembrane protein PRO1864.
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003095357-A1.
22-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM75139 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003104544-A1.
                                                                                                                                                                                                                                                                                                                                  Score 1195; DB 7;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
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                                                                        100.0%; Score 1195; DB 7;
100.0%; Pred. No. 1.3e-131;
                                                                                                                        ABM14934 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068766-Al.
        Human secreted polypeptide PRO1864, SEQ ID NO:66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA82501 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003049755-A1.
                                                                                                                                                                                                                                                     ABO41009 standard; protein; 234 AA.
Aman secreted/transmembrane protein (PRO) #33.
US2003068694-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB037349 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003068726-A1.
                                                                                                                                                                                                                                                                                                                                                                                    ABO36739 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003068715-A1.
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US2003049760-A1.
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13-MAR-2003.
(GETH ) GENENTECH INC.
Match ''...ity 100.0%;
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(GETH ) GENENTECH INC.
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JH ) GENENTECH I.

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Best Local Similarity 1

RESULT 442

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(GETH ) GENENTECH INC.
                             US2003068744-A1.
10-APR-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 443
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RESULT 438
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Best Local Similarity
RESULT 439
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(GETH ) GENF
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Length 234;
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      Score 1195; DB 7; Length 234; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM30858 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068771-A1.
10-APR-2003.
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Pred. No. 1.3e-131;
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(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

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ery Match 100.0%; Bred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABM31468 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068761-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                    nomszu/B standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US200306878-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1195; DB 7;
Pred. No. 1.3e-131;
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Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068713-A1.
                                                                                                                                                                                                                                                   Score 1195; DB 7;
Pred. No. 1.3e-131;
                                                     ABM31773 standard; protein; 234 AA.
Human secreted polypeptide PRO1864, SEQ ID NO:66.
US2003068680-A1.
10-APR-2003.
                                                                                                                      100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                        Human secreted polypeptide PRO1864, SEQ ID NO:66.
1052003068762-Al.
                                                                                                                                                                                                                                                                                                    ADBB5809 standard; protein; 234 AA. Human secreted/transmembrane protein (PRO) #33. US2003054472-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 234 AA
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10-APR-2003.
(GETH ) GENENTECH INC. 100.0%;
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03-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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10-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
          100.0%;
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US2003060600-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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US2003065161-A1.
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(GETH ) GENENTECH INC.
GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 450
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Best Local Similarity
RESULT 454
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RESULT 451
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                           Local Similarity
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Length 234;

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DDF95.3
Novel human secreted and transmembrane protein PRO1864.
US2003180795-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
ery Match
st Local Similarity 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted and transmembrane protein PRO1864, US2003207397-A1.
                                                         Novel human secreted and transmembrane protein PRO1864 US2003105298-A1. GS-7UN -2003. (GF-7UN -2003. (GF-7UN -2003. 100.0%; Score 1195; DB 7; Leng et Local Similarity 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                         ארספות protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
1052003018387-A1.
                                                                                                                                                                                                                                                                                                                                                                                            ADG08572 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180793-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG01241 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003207399-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF95416 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003207398-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG12231 standard; protein; 234 AA. Novel human secreted and transmembrane protein PRO1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH24046 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180918-A1.
25-SEP-2003.
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(GETH ) GENENTECH INC.
SEY MATCH 100.0%; SCORE 1195; DB 7;
Year Match 100.0%; Pred. No. 1.3e-131;
    Score 1195; DB 7;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                     Score 1195; DB 7;
Pred. No. 1.3e-131;
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(GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
    100.0%;
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PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%;
RESULT 470
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PA (GETH ) GENENTECH INC.

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Best Local Similarity 100.0%;

RESULT 467
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PA (GETH) GENENTECH INC.

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Best Local Similarity 100.0%;

RESULT 469
Query Match
Best Local Similarity
RESULT 465
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RESULT 471
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RESULT 472
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                                                                                                                                                                      Query Match 100.0%; Score 1195; DB 7; Length 234; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 457
                       Score 1195; DB 7; Length 234; Pred. No. 1.3e-131;
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Novel human secreted and transmembrane protein PRO1864.
US2003138882-A1.
24.JUL.2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC14847 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003073208-A1.
                                                                  nubyusyu standard, protein, 234 AA.
Novel human secreted and transmembrane protein PRO1864
US203083473-A1.
                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1195; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDI1311 standard; protein; 234 AA.
Human secreted/transmembrane PRO polypeptide #31.
US2003105013-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD37104 standard; protein; 234 AA.
Human secreted/transmembrane PRO polypeptide #31.
US2003105012-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD10351 standard; protein; 234 AA.

Human secreted/transmembrane PRO polypeptide #31
05-003105011-A1.
0 GFTH GENEWTECH INC.
100.0%; Score 1195; DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 461
ID ADD05539 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003087376-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADC17149 standard, protein; 234 AA.
Mammalian PRO polypeptide (SeqID 14).
US2003065143-A1.
                                                                                                                                                                                                                                                      ADC06970 standard; protein; 234 AA
                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
RESULT 459
                                                                                                                                                                                                                                                                         Human PRO1864 protein. US2003060602-A1.
                                                                                                                                                                                                                                                                                                               27-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                               01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
      (GETH ) GENENTECH INC
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                                            Best Local Similarity
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Best

Length 234;

Length 234;

Length 234;

Best Loca RESULT 464

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ADG85620 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180905-A1.
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Pred. No. 1.3e-131;
                                                                                                                     Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH14556 standard; protein; 234 AA.
ADH24556 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180907-A1.
                                                                                                                                                                                                                                                                                                        ADH23876 standard, protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180919-A1.
                                                                                                                                                        ADH29905 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180859-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG85280 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180904-A1.
25-SEP-2003.
                                   ADH34072 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180858-A1.
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted and transmembrane protein PRO1864.
US20031648-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
ery Match
St. Local Similarity 100.0%; Pred. No. 1.3e-131; St. Local Similarity 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                          Query Match 100.0%; Score 1195; DB 7; Best Local Similarity 100.0%; Pred. No. 1.38-131; RESULT 475
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100.0%; Pred. No. 1.3e-131;
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Human secreted and transmembrane protein PRO1864.
US2003181646-A1.
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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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Human PRO polypeptide #7.
US2003180837-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH08891 standard; protein; 234 AA. Human PRO polypeptide #33. US2003207395-A1.
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25-SEP-2003.
(GETH ) GENENTECH INC.
100.0%;
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%;
RESULT 477
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 480
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Best Local Similarity
RESULT 482
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                                                                                            25-SEP-200
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                        RESULT 474

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Score 1195; DB 7; Length 234; Pred. No. 1.3e-131;
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                         Length 234;
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Novel human secreted and transmembrane protein PRO1864.
US2003180920-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP27555 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180906-A1.
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Novel human secreted and transmembrane protein PRO1864.
US200180880-A1.
                                                                                                                                                                                                      ADH38510 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864 US2003181643-A1.
                                                                      ADH24216 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180914-A1.
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted and transmembrane protein PRO1864
US2003181649-A1.
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Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                     ADGB3631 standard; protein; 234 AA. Human PRO polypeptide #7. 25203180794-A1. 25-SEP-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%;
RESULT 492
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25-SEP-2003.
(GETH ) GENENTECH INC.
100.0%;
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Best Local Similarity 100.0%;
RESULT 491
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(GETH ) GENENTECH INC.
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25-SEP-2003.
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Best Local Similarity
RESULT 486
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Best Local Similarity
RESULT 488
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RESULT 489
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Length 234;

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ADI03384 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
                                                                                                                                    ADH89985 standard; protein; 234 AA. Novel human secreted and transmembrane protein PRO1864. US2003181697-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADI05034 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180848-A1.
25-SEP-2003.
(GETH) GENENTECH INC.
100.0%; Score 1195; DB 7; Lengt
Et Local Similarity 100.0%; Pred. No. 1.3e-131;
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Novel human secreted and transmembrane protein PRO1864
US2003181707-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH98216 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003181709-A1.
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PA (GETH) GENENTECH INC.

Query Match

100.0%; Score 1195; DB 7; Lengt

Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 508

ID ADH98046 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864

PN US2001181673-A1.

PA (GETH) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1864
US2003181708-A1.
Score 1195; DB 7;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 234 AA
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25-SEP-2003.
(GETH ) GENENTECH INC.
100.0%;
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PA (GETH ) GENENTECH INC.

QUETY MATCh

BEST Local Similarity 100.0%;

RESULT 503
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RESULT 504
ID ADIl1061 standard; protein;
DE Human PRO polypeptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO polypeptide #7.
US2003181684-A1.
25-SEP-2003.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                   Query Match
Best Local Similarity
RESULT 502
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RESULT 505
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RESULT 507
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RESULT 509
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RESULT 506
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                          Novel human secreted and transmembrane protein PRO1864.
US2003181636-A1.
                                                                                                                                                             ADH53661 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003181641-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH49852 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003181639-A1.
25-SEP-2003.
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Novel human secreted and transmembrane protein PRO1864
US2003181696-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003181698-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH97706 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003181672-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADI03554 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
                                                                                                                                                                                                                                                                                                                      ADH51997 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864 US2003181638-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003181669-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
                                               PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 493
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Human PRO polypeptide #7.
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25-SEP-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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RESULT 496
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(GETH ) GENENTECH INC.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 516
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        PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 511
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Novel human secreted and transmembrane protein PRO1864.
US2003181652-A1.
25-28P-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALHHUU325 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US200181699-A1.
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Novel human secreted and transmembrane protein PRO1864.
US2003181653-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003181674-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003190669-A1.
                                                                                             -__-ADI04779 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003181657-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003181676-A1.
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DE Human PRO polypeptide #7.

PN US2003181668-A1.

PD 25-SEP-2003.

PA (GETH) GENENTECH INC.

QUERY NATCh

Best Local Similarity 100.0%; Pred. N

RESULT 513
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Human PRO polypeptide #7.
US2003181666-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 519
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RESULT 517
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Length 234;
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Length 234;
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ID ADIO5208 standard; protein; 234 AA.

BR Novel human secreted and transmembrane protein PRO1864.

PD 25-SEP-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 1195; DB 7; Lengtl RESULT 528
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Novel human secreted and transmembrane protein PRO1864.
US2003191288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUJUS378 standard; protein; 234 AA. Novel human secreted and transmembrane protein PRO1864. US200316-A1.
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Novel human secreted and transmembrane protein PRO1864 US2003181675-A1.
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Novel human secreted and transmembrane protein PRO1864
US200181650-A1.
                                                             ADI03214 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003181655-A1.
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Pred. No. 1.3e-131;
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(GETH ) GENENTECH INC.
(ery Match 100.0%; Score 1195; DB 7;
ery Match 100.0%; Pred. No. 1.3e-131;
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PA (GETH ) GENENTECH INC.

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100.0%; Score 1195; DB 7;

Quenty Match

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RESULT 524
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
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Human PRO polypeptide #7.
US2003181685-A1.
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(GETH ) GENENTECH INC.
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Best Local Similarity 100.0%;
RESULT 526
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 521
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Best Local Similarity
RESULT 523
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                   Best Local Similarity RESULT 520
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ID ADI02303 standard;
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Pred. No. 1.3e-131

100.001

Best Local Similarity RESULT 538

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25-SEP-2003.
(GETH ) GENENTECH INC.
100.0%; Score 1195; DB 7; Length 234;
  Length 234;
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US2003181680-A1.
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Novel human secreted and transmembrane protein PRO1864.
US2003191289-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003171550-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003181670-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003181671-A1.
                                                                                                                                                                                                                         ADJULDIG Standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003181679-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003181651-A1.
                                                              ADI01446 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003181678-A1.
100.0%; Score 1195; DB 7; 100.0%; Pred. No. 1.3e-131;
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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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Human PRO polypeptide #7.
US2003181667-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADI01786 standard; protein; 234 AA
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 531
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    Query Match
Best Local Similarity
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Novel human secreted and transmembrane protein PRO1864.
US2002073813-A1.
ADK65384 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003073821-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                         ADL32672 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003207396-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC52152 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003130483-A1.
                                                                                                                                     ADH98726 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003191284-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL93698 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003040013-A1.
                                                                                                                                                                                                                                                                                               Novel human secreted and transmembrane protein PRO1864 US2003191287-A1.
                                                                                  Score 1195; DB 7;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                             Score 1195; DB 7;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                      Score 1195; DB 7;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Human secreted/transmembrane PRO polypeptide #31
US2003100497-A1.
29-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE74203 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33
US2003211572-A1.
                                                                                                                                                                                                                                                                                protein; 234 AA
                                                                                                                                                                                                                                                                                                               US2003121--
09-OCT-2003.
(GETH ) GENENTECH INC.
100.0%; SC
                                                                                                                                                                        US200312-1.
09-OCT-2003.
(GETH ) GENENTECH INC.
100.0%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
100.0%;
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10-JUL-2003.
(GETH ) GENENTECH INC.
100.0%;
                                                      17-APR-2003.
(GETH) GENENTECH INC.
100.0%;
277-11 cimilarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%;

Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2003.
(GETH ) GENENTECH INC.
100.0%;
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PA (GETH ) GENENTECH INC.

QUETY MATCh

Best Local Similarity 100.0%;

RESULT 543
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RESULT 540
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 541
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Best Local Similarity
RESULT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 545
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RESULT 539
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                                                                                                                                                                                                                                                                                  ADH79967 standard;
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Length 234;

Length 234;

Length 234;

RESULT 549

Best Loc RESULT 551

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uuery Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 558
                                                        100.0%; Score 1195; DB 8; Length 234; 100.0%; Pred. No. 1.3e-131;
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ADH06244 standard; protein; 234 AA.
US2003180854-A1.
25-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADH07948 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180845-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG69345 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180846-A1.
25-SEP-2003.
(GETH) GENENTECH INC.
ery Match
100.0%; Score 1195; DB 8; Lengt
Et Local Similarity 100.0%; Pred. No. 1.3e-131;
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Novel human secreted and transmembrane protein PRO1864.
US2003068770-A1.
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Novel human secreted and transmembrane protein PRO1864.
US2003166848-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH39166 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180917-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 04-SEP-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh

100.0%; SCORE 1195; DB 8;

BEST Local Similarity 100.0%; Pred. No. 1.38-131;

RESULT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1195; DB 8;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.
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US2003180842-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
100.0%; Score Juery Match similarity 100.0%; Pred. Need.
                                                                                                                                             ADG82715 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2003215910-A1.
CGETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                         ADH02341 standard; protein; 234 AA.
Human PRO polypeptide #7.
US2003180839-A1.
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%;
RESULT 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
RESULT 563
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Best Local Similarity 100.0%;
RESULT 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                               GENENTECH INC.
                                                        Query Match
Best Local Similarity
RESULT 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 561
      25-SEP-2003
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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         query Match 100.0%; Score 1195; DB 8; Length 234; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1195; DB 8; Length 234; 100.0%; Pred. No. 1.3e-131;
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DE Novel human secreted and transmembrane protein PRO1864.

PN US2003180913-A1.

PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG00459 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003215911-A1.
20-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADG04299 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003215912-A1.
20-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH06584 standard; protein; 234 AA. Novel human secreted and transmembrane protein PRO1864. US2003180852-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF06414 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180853-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG68835 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180855-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH27725 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180912-A1.
                                                                                                                                                                                                                     ADF96028 standard; protein; 234 AA. Novel human secreted and transmembrane protein PRO1864. US2003215909-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1195; DB 8; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 552
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1195; DB 8; 100.0%; Pred. No. 1.3e-131;
                                                                                                                             100.0%; Score 1195; DB 8; 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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ADE74815 standard; protein; 234 AA.
Human secreted/transmembrane protein (PRO) #33.
US2003211574-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH33698 standard, protein; 234 AA.
Human PRO polypeptide #7.
US2003181645-A1.
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Best Local Similarity 100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                       20-NOV-2003.
                                                                                                    13-NOV-2003.
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Best Local
                                                                                                                                Query Match
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Length 234;

Length 234;

5; DB 8; 1.3e-131;

Best Loca RESULT 555

RESULT 568

A D N G E

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Length 234;
  Length 234;
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Novel human secreted and transmembrane protein PRO1864.
US2003180849-A1.
                                                                                                                                                                                                                                                                                               ADG69685 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180843-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG85960 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180862-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH24896 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180909-A1.
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Novel human secreted and transmembrane protein PRO1864
                                                                                                                                                                                                                                                                                                                                                                      US.CS.--
25-SEP-2003.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH 100.0%; Score 1195; DB 8;
lery Match 100.0%; Pred. No. 1.3e-131;
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(GETH ) GENENTECH INC.
100.0%; Score 1195; DB 8;
EXY MATCh 100.0%; Pred. No. 1.3e-131;
100.0%; Score 1195; DB 8; 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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1 (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195;
                                                                      ADH01078 standard; protein; 234 AA. ADH01078 standard; protein; 234 AA. Human PRO polypeptide #7. US2003180838-A1. 25-SEP-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH02171 standard; protein; 234 AA.
Human PRO polypeptide #7.
US2003180841-A1.
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25-SEP-2003.
(GETH ) GENENTECH INC.
Wartch 100.0%; S.
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US2003180840-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
uery Match
est Local Similarity 100.0%; P
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25-SEP-2003.
(GETH ) GENENTECH INC.
100.0%;
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25-SEP-2003.
(GETH ) GENENTECH INC.
100.0%;
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PA (GETH) GENENTECH INC.
QUERY MATCh 100.0%;
Best Local Similarity 100.0%;
RESULT 580
  Query Match
Best Local Similarity
RESULT 575
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Best Local Similarity
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Best Local Similarity
RESULT 579
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RESULT 581
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                                                                                                                                                                                                                                          Best Local Similarity RESULT 576
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                               100.0%; Score 1195; DB 8; Length 234; 100.0%; Pred. No. 1.3e-131;
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                                                                Novel human secreted and transmembrane protein PRO1864. US2003180856-A1. 25-SP-2003. (GETH ) GENERAL INC.
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Novel human secreted and transmembrane protein PRO1864.
25-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                       Novel human secreted and transmembrane protein PRO1864.
US2003180910-Al.
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Novel human secreted and transmembrane protein PRO1864.
US2003180851.A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1864.
US2003180861-A1.
25-SEP-2003.
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Novel human secreted and transmembrane protein PRO1864
US2003180916-A1.
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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 567
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Pred. No. 1.3e-131;
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Human PRO polypeptide #7.
US2003181644-A1.
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Human PRO polypeptide #7.
US2003181637-A1.
                                                                                                                                                                                                                                                                                                                              ADH24386 standard; protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 234 AA
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US2003068768-A1.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC
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                                               Best Local Similarity RESULT 566
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Best Local Similarity
RESULT 569
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                               Query Match
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RESULT

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RESULT 596
RESULT 593
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                                                                                                                         Length 234;
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Novel human secreted and transmembrane protein PRO1864.
US2003180921-A1.
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Novel human secreted and transmembrane protein PRO1864.
US2003180857-A1.
                                  ADH07608 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180850-A1.
                                                                                                                                                                                                                                                                                                                     ADH24726 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003180908-A1.
25-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH57179 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003181642-A1.
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Novel human secreted and transmembrane protein PRO1864
US2003180922-A1.
                                                                                                                                                                           ADG86130 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180863-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH25774 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003180911-A1.
                                                                       PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 585
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PA (GETH ) GENENTECH INC.
Querry Match
100.0%; Score 1195; DB 8;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 591
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Pred. No. 1.3e-131;
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   100.0%; Pred. No. 1.3e-131
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US2003224984-A1.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                25-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 586
ID ADH24726 standard; pr
DE Novel human secreted
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC
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(GETH ) GENENTECH INC
 Best Local Similarity
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Best Local Similarity
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RESULT 588
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RESULT
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Length 234;
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Novel human secreted and transmembrane protein PRO1864.
US2003181703-A1.
25-SEP-2003.
(GETH) GENENTECH INC.
ery Match
to boal Similarity 100.0%; Pred. No. 1.3e-131;
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Novel human secreted and transmembrane protein PRO1864.
US2003187228-A1.
ADH90495 standard; protein; 234 AA.

Novel human secreted and transmembrane protein PRO1864.
US2003181700-A1.
25-SETP - 2003.
(GETH) GENENTECH INC.
100.0%; Score 1195; DB 8; Lengt
EL Local Similarity 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                        AUHYSBY6 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003190698-A1.
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Novel human secreted and transmembrane protein PRO1864
US200181701-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ98540 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
US2003187197-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI02126 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003190699-A1.
                                                                                                                                                                                                         25-SEF-zous.
(GETH ) GENENTECH INC.
iry Match 100.0%; Score 1195; DB 8;
iry Match 100.0%; Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
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                                                                                                                                              protein; 234 AA
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09-OCT-2003.
(GETH ) GENENTECH INC.
"" DECTH ) GENENTECH INC.
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02-007-2003.
(GETH ) GENENTECH INC.
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%;
RESULT 599
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RESULT 600
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Human PRO polypeptide #7.
US2003181683-A1.
25-SEP-2003.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 602
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SULT 598
                                                                                                   Best Local Similarity RESULT 594
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Best Local Similarity
RESULT 597
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RESULT 595
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Best Local Similarity
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                                                                                               Query Match
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Novel human secreted and transmembrane protein PRO1864
                    US2004053358-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 8; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 234;
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                                                                                               Length 234;
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                                                                                                                                                                                                                                                      Length 234;
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ADJ99103 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864.
                                                                                                                                                                                                                                                                                                           ADJ98891 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003187242-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH79039 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003181702-A1.
C55-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK14420 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2003187229-A1.
                                                                                                                                                                         Novel human secreted and transmembrane protein PRO1864
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1195; DB 8; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1195; DB 8; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1195; DB 8; Best Local Similarity 100.0%; Pred. No. 1.3e-131; RESULT 610
                                                                                               100.0%; Score 1195; DB 8; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1195; DB 8; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                  100.0%; Score 1195; DB 8; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK00899 standard; protein; 234 AA.
Human PRO polypeptide #7.
US2003186407-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK82840 standard; protein; 234 AA. Human PRO polypeptide #31. US2004043927-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ64475 standard; protein; 234 AA.
Human PRO polypeptide #33.
US2004038337-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM36418 standard; protein; 234 AA
                                                                                                                                                       ADJ99273 standard; protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-2004.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                        02-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2003.
(GETH ) GENENTECH INC
                                                                                                           Best Local Similarity RESULT 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 605
                                                                                                                                                                                                                                                                  Local Similarity
                                        US2003186408-A1.
                                                                                                                                                                                              US2003187196-A1.
                                                                                            Query Match
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Length 234;
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                                        Length 234;
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Pred. No. 8.5e-131;
                                                                                            ADM4023 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2004048335-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN37831 standard; protein; 234 AA.
Novel human secreted and transmembrane protein PRO1864
US2004091959-A1.
                                                                                                                                                       PD 11-MAR-2004.

PA (GETH ) GENENTECH INC.

QUEATY MATCh 100.0%; Score 1195; DB 8;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 613
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24-CT-2002.
(INCY-) INCYTE GENOMICS INC.
100.0%; Score 1195; DB 6;
lery Match
100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                        Score 1195; DB 8;
Pred. No. 1.3e-131;
                                      Score 1195; DB 8;
Pred. No. 1.3e-131;
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Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1195; DB 8;
Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1195; DB 4; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1195; DB 4; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP75508 standard; protein; 238 AA.
Human secretory polypeptide SPTM SEQ ID NO 692.
WO200283876-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM41716 standard; protein; 238 AA.
Human polypeptide SEQ ID NO 6647.
WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM41715 standard; protein; 238 AA.
Human polypeptide SEQ ID NO 6646.
WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM39930 standard; protein; 216 AA.
Human polypeptide SEQ ID NO 3075.
                                                                                                                                                                                                                                                                                                                                                                                                                 ADL91873 standard; protein; 234 AA.
Human PRO1864 protein SEQ ID NO:94.
WO2004024076-A2.
                                                                                                                                                                                                                                                            protein; 234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR58404 standard; protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                      100.0%;
PD 18-MAR-2004.

PA (GETH ) GENENTECH INC.

QUETY Match 100.0%;

Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 13-MAY-2004.

PA (GETH ) GENENTECH INC.

Query Match 100.0%;

Best Local Similarity 100.0%;

RESULT 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.4%;
                                                                                                                                                                                                                                                                            Human PRO polypeptide #7.
US2004058411-A1.
25-MAR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 618
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Best Local Similarity
RESULT 619
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RESULT 620
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                          ADM80869 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOV19b.
WO2003029423-A2.
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RESULT 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.0%; Score 669.5; DB 7; Length 176; 87.5%; Pred. No. 5.7e-70;
                                                                                                                                                                                                   Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 664; DB 8; Length 445; Pred. No. 9.1e-69;
                                                       91.8%; Score 1097; DB 4; Length 216; 92.3%; Pred. No. 3.9e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.0%; Score 777; DB 4; Length 283; 72.5%; Pred. No. 2.5e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 445;
                                                                                                                                                                                                                                                                                                                                        Score 985; DB 6; Length 198;
Pred. No. 5.1e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR47530 standard; protein; 445 AA.
Breast cancer associated protein sequence SEQ ID NO:296.
WO2003004989-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH13184 standard; protein; 445 AA.
Human malignant neoplasia-related protein SeqID33
EP1365034-A2.
                                                                                                                                                             GS-NOV-2001.

(HUMA-) HUMAN GENOME SCI INC.

(HUMA-) HUMAN GENOME SI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD 20-FEB-1997.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
PA (CANS.) CENT NAT RECH SCI.
PA (UTAS.) CENT NAT RECH SCI.
PA (UTAS.) UNIV PASTEUR LOUIS.
PA (BRIM.) BRISTOL-MYERS SQUIBS. CO.
Query Match
Best Local Similarity 55.6%; Score 664; DB 2;
RESULT 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%; Score 665; DB 5; 91.0%; Pred. No. 1.5e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.6%; Score 664; DB 6; 56.2%; Pred. No. 9.1e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB64413 standard; protein; 176 AA.
Human protein encoded by clone FEBRA20007820.
EP1308459-A2.
                                                                                                        ABB90287 standard; protein; 201 AA. Human polypeptide SEQ ID NO 2663. WO200190304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK36828 standard; protein; 146 AA.
Novel human polypeptide SeqID8910.
WO200216439-A2.
28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW25768 standard; protein; 445 AA.
Human MLN 64.
W09706256-A2.
                                                                                                                                                                                                                                                                                                                                                                                            AAU30250 standard; protein; 283 AA.
Novel human secreted protein #741.
WO200179449-A2.
                                                                                                                                                                                                                                                        ABR58403 standard; protein; 198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.6%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-2003.
(MILL-) MILLENIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cer as

JO4989-A2.

JAN-2003.

(MILL-) MILLENIUM Ph.

Query Match

Best Local Similarity 5.

RESULT 628

ID ADH13184 stand?

DE Human malire

PN EP1365^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 625
ID ADK36828 standard; pr
DE Novel human polypepti
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                           10-APR-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 622
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                        Best Local Similarity RESULT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2001.
(HYSE-) HYSEQ INC.
                          26-JUL-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                             Human NOV19a.
WO2003029423-A2.
         WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-2003
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AAB96837 standard; protein; 424 AA.
Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.
PR2792651-A1.
CONT-2000.
(CNRS ) CNRS CENT NAT RECH SCI.
(IRRE) IFREMBR INST PR RECH EXPL MER.
(IFRE) STANDAR INST PR RECH EXPL MER.
SETY MATCH
SETY MATCH
SET LOCAl Similarity 21.9%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                            33.9%; Score 405.5; DB 6; Length 111; 73.7%; Pred. No. 3.4e-39;
                                                                                                Score 625; DB 4; Length 534;
Pred. No. 4.6e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 580;
                                                                                                                                                                                                                                                                   Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-2001.
A (MICR-) MICROBIAL TECHNICS LTD.
Query Match
Best Local Similarity 25.7%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 91; DB 5; Length 651; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEXALL AAM901384 standard; protein; 70 AA.

ID AAM901384 standard; protein; 70 AA.

DE Human immune/haematopoietic antigen SEQ ID NO:17977.

DE WO200157182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

QUERY Match

Best Local Similarity 98.4%; pred. No. 1.2e-29;

RESULT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB59968 standard; protein; 580 AA.
Drosophila melanogaster polypeptide SEQ ID NO 6696.
W2020171042-A2.
27-SEP-2001.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU03699 standard; protein; 373 AA.
Group B Streptococcus antigenic protein, ID-176
W0200132882-A2.
                                                                                                                                                                                                                                                                                                                         ABP75900 standard; protein; 111 AA.
Human secretory polypeptide SPTM SEQ ID NO 1084
W02002816-A2.
24-0CT-2002.
(INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.7%; Score 343; DB 4; 37.8%; Pred. No. 7.6e-31;
                                                                                                                                                                                                                                                               48.4%; Score 578; DB 6; 58.3%; Pred. No. 1.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus polypeptide SEQ ID NO 9810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus polypeptide SEQ ID NO 8640.
ABG05498 standard; protein; 534 AA.
Novel human diagnostic protein #5489.
WO200175067-A2.
                                                                                                                                                          ABR69622 standard; protein; 412 AA.
Human CGDD-22 protein.
WO2003027263-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 7.6%;
Local Similarity 25.7%;
                                                                                                    52.3%;
                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-2002.
(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity RESULT 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                    Query Match
Best Local Similarity
RESULT 630
                                                              11-OCT-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                   03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                        Query Match
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Query Match 7.2%; Score 85.5; DB 2; Length 438; Best Local Similarity 25.5%; Pred. No. 1; RESULT 647
                                                                                                                                                                                                                                                        DB 2; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 85.5; DB 6; Length 440;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 85.5; DB 8; Length 440;
Pred. No. 1;
                                                                 Batten disease CLN3 mutant protein; 438 AA.
WO9708308-A1.
OG-MAR-1997.
                                                                                                                                                                                                                                                      Score 85.5;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN63244 standard; protein; 440 AA.
Human NOV43a variant.
US2004038223-A1.
                                                                                                                                                                                                                                                                                                                             ADA05822 standard; protein; 440 AA. Human NOV43a protein SEQ ID NO:182.WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 650
ADN62985 standard; protein; 440 AA
                                                                                                                                                                                                                                                   Query Match 7.2%;
Best Local Similarity 25.5%;
RESULT 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.2%;
Best Local Similarity 25.2%;
RESULT 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 7.2%;
Local Similarity 25.2%;
                                                                                                                                                                                                    (GEHO ) GEN HOSPITAL CORP. (UYLE-) RIJKSUNIV LEIDEN.
(UYLE-) RIJKSUNIV LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                                                                                                                                                                                                                                                                                                                         10-APR-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GUO X.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS2004038223-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZHONG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NOV43a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIEG/)
(SPAD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LILL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEYM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LILL/)
(GUOX/)
(PATT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELLE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RAST/)
(STON/)
(PENA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SHIM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIPI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EISE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEYM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KEKU/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7000/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GORTT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZERH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANDE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (/NOHZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JIWW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SHEN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEKU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SPYT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEAC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (מממי)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT | 110 AD | 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AABS8945 standard; protein; 516 AA.
Breast and ovarian cancer associated antigen protein sequence SEQ ID 653.
WO200055173-A1.
21-SEP-2000.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2003.

4 (INCY-) INCYTE GENOMICS INC.

Query Match

Best Local Similarity 25.5%; Pred. No. 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D 03-OCT-2002.
A (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 21.0%; Pred. No. 0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 7.2%; Score 85.5; DB 2; Length 438; Local Similarity 25.5%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.3%; Score 87.5; DB 3; Length 516; 25.2%; Pred. No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 155
     DB 5; Length 654;
                                                                                                                                                                                                                                 DB 5; Length 654;
                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 80037.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG59838 standard; protein; 155 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 77441.
EP1033405-A2.
06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU26680 standard; protein; 396 AA.
Protein encoded by Prokaryotic essential gene #12207.
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW13589 standard; protein; 438 AA.
Batten disease CLN3 mutant protein in family L204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW13582 standard; protein; 438 AA.
Batten disease CLN3 mutant protein in family L46.
W09708308-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 7.3%; Score 87.5; DB 3; Local Similarity 21.4%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 87.5; DB 3;
Pred. No. 0.14;
                                                                                                                        WO20023-...
02-MAY-2002.
02-MAY-2002.
(GEIR-) CHRENON SPA.
(GENO-) INST GENOMIC RES.
7.6%; Score 91; DB 5.
7.6%; Pred. No. 0.4;
Query Match 7.6%; Score 91; DB Best Local Similarity 25.7%; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 85.5; 24.8%; Pred. No. 1;
                                                                    ABP26469 standard; protein; 654 AA.
Streptococcus polypeptide SEQ ID NO 2114.
WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW13575 standard; protein; 438 AA.
Batten disease polypeptide CLN3.
WO9708308-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE28099 standard; protein; 340 AA.
Human NTRAN protein - SEQ ID 4.
WO2003051902-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.3%;
Best Local Similarity 21.4%;
RESULT 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-1997.
(GEHO ) GEN HOSPITAL CORP.
(UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEHO ) GEN HOSPITAL CORP. (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAR-1997.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9708308-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 641
ID AABS89
DE Breast
PN WO2000
PD 21-SEE
PA (HUMA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 643
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AAG53771 standard; protein; 322 AA.
              06-MAR-1997.
(GEHO ) GEN HOSPITAL CORP.
(UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 663
                                                                                                                                                              Best Local Similarity RESULT 658
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 659
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 660
                                                       Query Match
Best Local Similarity
RESULT 657
                                                                                                                                                                                                                                       11-OCT-2001.
(HYSE-) HYSEQ INC.
WO9708308-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-1997
                                                                                                                                                                                                                                                                                                                                                   03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 84.5; DB 6; Length 430;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 656
                                                                                                                                                                                                                                                                                                                                                                                 Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.2%; Score 85.5; DB 2; Length 467; 25.5%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Length 500,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ18055 standard; protein; 473 AA.
Human soft tissue sarcoma-upregulated protein - SEQ ID
WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU40544 standard; protein; 500 AA.
ADVOLEIN encoded by Prokaryotic essential gene #26071.
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU33210 standard; protein; 430 AA.
Protein encoded by Prokaryotic essential gene #18737,
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW13588 standard, protein; 438 AA.
Batten disease CLN3 mutant protein in family L10.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAWI3593 standard; protein; 467 AA.
Batten disease CLN3 mutant protein in family L61
W09708308-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.2%; Score 85.5; DB 8; Best Local Similarity 25.2%; Pred. No. 1.1; RESULT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                     DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85.5; DB Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.2%; Score 85.5; Di 25.2%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                    Score 85.5;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABBB9640 standard; protein; 473 AA. Human polypeptide SEQ ID NO 2016. WO200190304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-2004.
(PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD 03-0CT-2002.
PD 03-0CT-2002.
PA (ELIT-) ELITRA PHARM INC.
QUELY MATCH
BEST Local Similarity 26.0%; Pr.
RESULT 655
ID ABU3310 Stand---
DE Pref. 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 25.2%;
RESULT 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAR-1997.
(GEHO ) GEN HOSPITAL CORP.
(UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                        MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHENOY S G.
SHENOY S H.
ROTHENBERG M E.
LEACH M D.
                                                                                                                                                                                                                                                                                      (AGEE) AGEE M L.
(BERG) BERGES C.
(DIPL) DIPIPPO V A.
(EISE) EISEN A.
(GANG) GANGOLLI E A.
(RIEG) RIEGER D K.
(SPAD) SPADERNA S K.
                       SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                         GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
          PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 653
                                                                                                                                   ZHONG M.
CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
        (PATT/)
(SPYT/)
                                                                (MALY/)
                                                                                                                        (ANDE/)
                                                                                                                                                                                                                                    SHEN/)
                                                                                             GORM/
                                                                                                                                                   CATT/
                                                                                                            ZERH/
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ADE28193 standard; protein; 577 AA.
ADE28193 standard; protein; 577 AA.
HUMAN MDDT protein - SEQ ID 43.
WO2003046152-A2.
05-JUN-2003.
GINCY-D INCYTE GENOMICS INC.
6.8%; Score 81.5; DB 7; Length 577;
ery Match
st Local Similarity 22.6%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.8%; Score 81.5; DB 4; Length 519;
Best Local Similarity 22.6%; Pred. No. 3.8;
RESULT 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 81.5; DB 2; Length 438;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82.5; DB 2; Length 438;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                     DB 4; Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 239;
Length 438;
                                                                                                                                  Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82; DB 7; Length 589;
Pred. No. 3.9;
                                                          AAG16921 standard; protein; 322 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 17749.
EP103405-82.
                                                                                                                                                                                                                                                                                                                                            ABU35608 standard; protein; 239 AA.
AProtein encoded by Prokaryotic essential gene #21135.
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -AMN13590 standard; protein; 438 AA.
Battan disease CLN3 mutant protein in family L216.
WO9708308-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW13586 standard; protein; 438 AA.
Batten disease CLN3 mutant protein in family L285.
W09708308-A1.
                                                                                                                                Score 83.5; DB 3;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                            9
  Score 84.5; DB 2;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 82.5; DB
Pred. No. 0:99;
                                                                                                                                                                                                                                                                                       7.0%; Score 83.5; Di
20.1%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- AAB52924 standard; protein; 519 AA. AAB52924 standard; protein sequence SEQ ID NO:11574. EP1074617-A2.
                                                                                                                                                                                         AG21285 standard; protein; 472 AA.
Novel human diagnostic protein #21276.
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB85263 standard; protein; 589 AA.
Mouse RNA1 homologue SEQ ID NO:144.
EP1284297-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            6.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 19-FEB-2003.
PA (WARN ) WARNER LAMBERT CO.
Query Match
Best Local Similarity 19.5%;
RESULT 662
                                                                                                                                      7.0%;
      7.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GE-MAR-1997.
(GEHO ) GEN HOSPITAL CORP.
(UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP. (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2001.
(HELI-) HELIX RES INST.
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ADL/7926 standard; protein; 360 AA.
Albumin fusion protein related therapeutic protein X, SEQ ID No 1308.
US2004010134-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE03831 standard; protein; 360 AA.
Human gene 14 encoded secreted protein HDQFN31, SEQ ID NO: 77.
WO200136440-A1.
Score 80; DB 3; Length 144;
Pred. No. 0.96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2001.
(HUWA-) HUMAN GENOME SCI INC.
HERY Match 6.7%; Score 80; DB 4; Length 360;
                                                                                                                                                  6.7%; Score 80; DB 4; Length 238; 22.5%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                               6.7%; Score 80; DB 7; Length 238; 22.5%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WULLY MAICH 6.7%; Score 80; DB 6; Length 330; Best Local Similarity 24.6%; Pred. No. 3; RESULT 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU25554 standard; protein; 365 AA.
Protein encoded by Prokaryotic essential gene #11081.
WO200277183-A2.
93-OCT--2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM67388 standard; protein; 330 AA.
Photorhabdus luminescens protein sequence #485.
                                                                                                                                                                                         Human protein; 238 AA. Epistein; 238 AA. Epistein of the invention SEQ ID NO:3158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WCACT-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
6.7%; Score 80; DB 5
6.7% MAtch
7.milarity 22.5%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.7%; Score 80; DB 422.5%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 80; DB (
Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR77844 standard; protein; 309 AA.
Molasses toxicity resisitance protein RIM1.
WO9514774-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80; DB :
Pred. No. 2.8;
                                                    AAM39952 standard; protein; 238 AA. Human polypeptide SEQ ID NO 3097. W0200153312-A1. C4-UUL-2001. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                       AAM41738 standard; protein; 249 AA.
Human polypeptide SEQ ID NO 6669.
WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG64559 standard; protein; 360 AA.
Human albumin fusion protein #1234.
WO200177137-A1.
                                                                                                                                                                                                                                                            24-SEP-2003,
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-2002.
(INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO95JU-1995.
01-JUN-1995.
(CNRS ) CENT NAT RECH SCI.
 6.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 681
                                                                                                                                                                  Best Local Similarity RESULT 676
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Best Local Similarity
RESULT 682
   Query Match
Best Local Similarity
RESULT 675
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Best Local Similarity
RESULT 677
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Best Local Similarity
RESULT 679
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Best Local Similarity
RESULT 678
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                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200294867-A2.
                                                                                                                                                    Query Match
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Human pancreatic cancer antigen protein sequence SEQ ID NO:851
WO200055320-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 350;
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                                                           Length 322;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD43870 standard; protein; 536 AA.
Chlamydia trachomatis immunogenic protein, SEQ ID No 165.
N W02003049762-A2.
D 19-JUN-2003.
A (CHIRON SPA.
GUBTY MAtch
GUBTY MAtch
   Arabidopsis thaliana protein fragment SEQ ID NO: 68491
EP1033405-A2.
                                                                                                                                                                                                                                                                68457
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Protein encoded by Prokaryotic essential gene #18563.
WO200277183-A2.
                                                                                                             AAG25639 standard; protein; 322 AA.
Arabidopsis thaliana protein fragment SEQ ID NO:
EP1033405-A2.
                                                                                                                                                                                                                           AAG53746 standard; protein; 322 AA.
Arabidopsis thaliana protein fragment SEQ ID NO:
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.7%; Score 80.5; DB 5;
Best Local Similarity 19.0%; Pred. No. 4.2;
RESULT 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 80.5; DB 7;
Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                    Score 80.5; DB 3;
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 80.5; DB 6;
Pred. No. 4.2;
                                                         Score 80.5; DB 3;
Pred. No. 2.6;
                                                                                                                                                                                       Score 80.5; DB 3;
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC42920 standard; protein; 891 AA.
Vaccinia Virus Major Core protein P4a precursor.
W02003017943-A2.
06-WARA-2003.
(MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB92830 standard; protein; 1780 AA.
Herbicidally active polypeptide SEQ ID NO 2041.
WO200210210-A2.
                                                                                                                                                                                                                                                                                                                                                                    ABO63194 standard; protein; 350 AA.
Klebsiella pneumoniae polypeptide segid 9711.
US6610836-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.7%; Score 80.5; Di
25.2%; Pred. No. 5.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.7%; Score 80.5; 1
20.8%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 80.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB48552 standard; protein; 463 AA.
Listeria monocytogenes protein #1256.
WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-2003.
(GENO-) GENOME THERAPEUTICS CORP.
lery Match
---- cimilarity 31.8%; Scor
                                                                                                                                                                                                                                                                                                                      6.7%;
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                                                           6.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) 18-OCT-2001.
(INSP ) INST PASTEUR.
Query Match
                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 671
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                                                      Query Match
Best Local Similarity
RESULT 666
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Best Local Similarity
RESULT 668
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Best Local Similarity
RESULT 669
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                                          06-SEP-2000.
                                                                                                                                                                       06-SEP-2000.
                                                                                                                                                                                                                                                                                                     06-SEP-2000.
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Query Match

Query Match

Query Match Best Loca RESULT 674

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6.7%; Score 79.5; DB 2; Length 406; 19.3%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 723;
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(EOSB-) EOS BIOTECHNOLOGY INC.
17Y Match
17 Match (6.6%; Score 79; DB 6; Length 1531;
17 Incal Similarity 24.3%; Pred. No. 33;
                          Score 79.5; DB 6; Length 365;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 638;
                                                                                                                                                                                                                                                                                    DB 2; Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.6%; Score 79; DB 4; Length 323; 18.8%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.6%; Score 79; DB 2; Length 121; 21.4%; Pred. No. 0.99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW20696 standard; protein; 121 AA.
H. pylori secreted or periplasmic protein 05ae20220orf50.
WO9640893-A1.
                                                                                                                                                                                                                                                                                                                                                                                AAW27275 standard; protein; 406 AA.
Human cytomegalovirus immediate-early exon 4 product
W09740165-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB60462 standard; protein; 323 AA.
Drosophila melanogaster polypeptide SEQ ID NO 8178.
W0200171042-A2.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB54483 standard; protein; 638 AA.
Drosophila melanogaster polypeptide SEQ ID NO 2241
W0200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL12774 standard; protein; 723 AA.
Human steroid-induced C3A liver cell protein #80.
US6673549-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE13277 standard; protein; 723 AA. Human transporters and ion channels (TRICH)-4. WO200177174-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
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Human cancer related protein SEQ ID NO:267.
WO2003025138-A2.
27-MAR-2003.
                                                                                                                                                                                                                                                                   Lucry Match 6.7%; Correct Disease Local Similarity 19.3%; Pred. No. 4.6; RESULT 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 79.5; I
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2001.
(INCY-) INCYTE GENOMICS INC.
ery Match
er Local Similarity 18.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1997.
(WIST-) WISTAR INST ANATOMY & BIOLOGY.
                                                                                                                                                                                                                               18-AUG-1994.
(WIST-) WISTAR INST ANATOMY & BIOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE31753 standard; protein; 1531 AA.
Human 59590 protein #SEQ ID 110.
WO2003065984-A2.
                                                                                                                      AARS8703 standard; protein; 406 AA.
HCMV IE-exon-4 subunit.
WO9417810-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.78;
18.08;
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                          6.7%;
(ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CEST TO THE CONTROL OF THE CONTROL O
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LO01.

ACT DE CORP NY.

LOCAL Similarity 1

RESULT 691

ID ABR58610 standa

DE Human cance

PN WO2030*

PD 27-**
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Jayabal.

JAN-2004.

(INCY-) INCYTE CORP.

Query Match

Best Local Similarity 1

RESULT 699

ID AAW20696 stand? DE H. Pylori P.

PN W09640P*

PN W09640P*
                             Query Match
Best Local Similarity
RESULT 684
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Best Local Similarity
RESULT 687
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Best Local Similarity
RESULT 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001.
(PEKE ) PE CORP NY.
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(CHIR) CHIRON SPA.

(CHIRO) INST GENOMIC RES.

Query Match

Best Local Similarity 23.5%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.6%; Score 78.5; DB 6; Length 239; Best Local Similarity 23.4%; Pred. No. 2.9; RESULT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%; Score 78.5; DB 5; Length 669; 23.5%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 228
                                                                                                                                            6.6%; Score 79; DB 6; Length 1597; 24.3%; Pred. No. 35;
                                                                                                                                                                                                                                                                                           Length 1597;
6.6%; Score 79; DB 7; Length 1531; 24.3%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU36298 standard; protein; 239 AA.
Protein encoded by Prokaryotic essential gene #21825.
W0200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB10816 standard; protein; 228 AA.
Albiococcus otitis antigenic protein SEQ ID NO:4244
WOZ010348304-AZ.
IZ-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6%; Score 78.5; DB 6; 22.5%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                   Human genome derived single exon protein #1923. US2003194704-A1.
                                                                                                                                                                                                                                                                                                 . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 78.5; Di
59.4%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                               , DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 78.5; I
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP29904 standard; protein; 669 AA.
Streptococcus polypeptide SEQ ID NO 8984.
WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP28724 standard; protein; 669 AA. Streptococcus polypeptide SEQ ID NO 6624.WO20023471-A2.
                                                                                                                                                                                                                                                                                               Score 79;
Pred. No.
                                                                                                                                                                                                      ABUG2070 standard; protein; 1597 AA. Mouse heart alpha-kinase (HK). US2002177205-Al. 28-NOV-2002.
                                                     ABU62069 standard; protein; 1597 AA.
Human heart alpha-kinase (HK).
US2002177205-A1.
(RYAZ/) RYAZANOV A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADIZ1047 standard; protein; 703 AA. Novel human protein #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ab027174 standard; protein; 626 AA. Human TRICH-6, SEQ ID 6. WO20040123-A2. 12-FEB-2004. (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.6%;
Best Local Similarity 18.0%;
                                                                                                                                                                                                                                                                                               6.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMHP ) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2002.
(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 696
                                                                                                                                                                                                                                                                                                                                                                                                                           (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                   Best Local Similarity
RESULT 693
                                                                                                                                              Query Match
Best Local Similarity
RESULT 694
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 697
                                                                                                                                                                                                                                                                                (RYAZ/) RYAZANOV A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2003
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         Query Match
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RESULT 70
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A B B B B

PBZGG

BBBBB

A G E E

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03-CCT-ZUUZ.
(ELIT-) ELITRA PHARM INC.
iry Match
6.5%; Score 77.5; DB 6; Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.5%; Score 77.5; DB 4; Length 280; 21.9%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.5%; Score 77.5; DB 6; Length 280; 21.9%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.5%; Score 77.5; DB 2; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 77.5; DB 5; Length 269;
Pred. No. 4.5;
                                                                                                                                                                                                        AAU35545 standard; protein; 471 AA.
Haemophilus influenzae cellular proliferation protein #186
WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 489;
9;
               DB 3; Length 377;
                                                                                                                                                Score 78; DB 3; Length 442;
Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                       DB 4; Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG20803 standard; protein; 489 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 23129.
BP1031405-A2.
06-SEP-2000.
                                                                     AAG20804 standard; protein; 442 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 23130.
EP1033405-A2.
6-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                             ABU30411 standard; protein; 471 AA.
Protein encoded by Prokaryotic essential gene #15938.
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 327 AA.
Prokaryotic essential gene #34416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW13576 standard; protein; 438 AA.
Mouse Batten disease polypeptide CLN3 homologue.
WO9708308-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO00771 standard; protein; 280 AA.
Polypeptide encoded by novel human contig #22.
WO2003023013-A2.
                 Score 78; DB 3
Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                     Score 78; DB 4
Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78; DB (
Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG17374 standard; protein; 280 AA.
Novel human diagnostic protein #17365.
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria monocytogenes protein #1743.
WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB49039 standard; protein; 269 AA.
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27-SEP-2001.
(ELIT-) ELITRA PHARM INC.
Perv Match ....larity 25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          WOZOCZ

WOZOCZ

(BLIT-) ELITRA PHARM INC.

(ELIT-) ELITRA PHARM INC.

6.5%;
                 6.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAR-1997.
(GEHO ) GEN HOSPITAL CORP.
(UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2001.
(INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
RESULT 719
               Query Match
Best Local Similarity
RESULT 711
                                                                                                                                                  Query Match
Best Local Similarity
RESULT 712
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RESULT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 714
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Best Local Similarity
RESULT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU48889 standard;
Protein encoded by
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-2003.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-200;
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  AAE02441 standard; protein; 766 AA.

Human ATP binding cassette, ABCB9 transporter protein mutant K545R.
W0200140305-A1.
07-JUN-2001.
(ACTI-) ACTIVE PASS PHARM INC.
6.6%; Score 78.5; DB 4; Length 766;
Et Local Similarity 18.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE02442 standard; protein; 766 AA.
Whaman AFP binding cassette, ABCB9 transporter protein mutant D667N.
WO200140305-A1.
07-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG67163 standard; protein; 766 AA.
Amino acid sequence of a human 33894 transporter polypeptide
WO200164875-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG79246 standard; protein; 766 AA.
Amino acid sequence of a human TAP-like (HUTAPL) polypeptide
WO200173018-A2.
                                                     DB 7; Length 703;
                                                                                                                                                                                                                                                                                                                                       Query Match 6.6%; Score 78.5; DB 4; Length 766; Best Local Similarity 18.0%; Pred. No. 15; RESULT 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 78.5; DB 4; Length 766;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.6%; Score 78.5; DB 5; Length 766; Best Local Similarity 18.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 766;
                                                                                                                                                                                                          Length 723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                           ABP52105 standard; protein; 723 AA.
Homo sapiens ABC transporter ABCB9 protein SEQ ID NO:57.
EP1217066-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG20805 standard; protein; 377 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 23131.
BP1033405-A2.
                                                                                                                                                                                                                                                      E Human ATP binding cassette, ABCB9 transporter protein.

N WO200140305-A1.

N D 07-JUN-2001.

A (ACTI-) ACTIVE PASS PHARM INC.

Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                          Score 78.5; DB 5;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                       Score 78.5; I
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.6%; Score 78.5; 1
18.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 78.5; 1
18.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 6.6%; Score 78.5; Local Similarity 18.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB98145 standard; protein; 766 AA.
Human ABC transporter ABCB9 SEQ ID NO 6.
WO200264781-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB21170 standard; protein; 766 AA
Human TRICH-14 protein.
WO200212340-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2002.
(ACTI-) ACTIVE PASS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; S
Best Local Similarity 18.0%; P
RESULT 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001.
(MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                          6.6%;
18.0%;
                                                       6.6%;
18.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MERE ) MERCK PATENT GMBH.
Query Match 6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2002.
(INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 708
                                                   Query Match
Best Local Similarity
RESULT 702
                                                                                                                                                                                                                        Best Local Similarity
RESULT 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
               27-MAR-2003.
(HYSE-) HYSEQ INC.
                                                                                                                                                                      26-JUN-2002.
(UYGE-) UNIV GENT.
WO2003025148-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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RESULT 707
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27.5%; Pred. No. 18;

Best Local Similarity RESULT 729

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Length 892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.4%; Score 77; DB 6; Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4%; Score 77; DB 7; Length 383; 24.8%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 77; DB 3; Length 648;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.4%; Score 77; DB 6; Length 650; 27.5%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 353; 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.4%; Score 77; DB 8; Length 353; 22.1%; Pred. No. 7.5;
                                                                                                                                                                                                                                                      DB 2; Length 353;
                                                                                                                                                                                                                                                                                                                                                                                       Score 77; DB 2; Length 353;
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG42221 standard; protein; 648 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 53040.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABUIG172 standard; protein; 650 AA.
Protein encoded by Prokaryotic essential gene #1699.
W0200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM25403 standard; protein; 383 AA.

Hyperthermophile Methanopyrus kandleri protein #9.
W02003076575-A2.
18-SEP-2003.
(FIDE. PIDELITY SYSTEMS INC.
(MALY.) MALYKH A.
                                                                                                                    DB 7;
                                                                                                                                                                                                    PD 28-DEC-1995.

PA (MASS-) MASSACHUSETTS GEN HOSPITAL.

Query Match

Goety Match

Goety Match

Best Local Similarity 22.1%; Pred. No. 7.5;
8.9;
                                                                                                                   6.5%; Score 77.5; I
22.7%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.4%; Score 77; 22.1%; Pred. No.
27.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM72713 standard; protein; 650 AA. Staphylococcus aureus protein #1953. W0200294868-A2. 28-N0V-2002. (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB07571 standard; protein; 353 AA. Mouse melatonin 1a (Mella) receptor US6326526-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AD029553 standard; protein; 353 AA. Mouse GPCR WINRIA, SEQ ID NO:655. W0200440000-A2.
                                                                                                                                                                     AAR88413 standard; protein; 353 AA.
High-affinity melatonin-la receptor
WO9535320-A1.
                            AD042919 standard; protein; 892 AA.

E Variola smallpox virus Al0L.

N W02003017943-A2.

O 6-MAR-2003.

MYRIAD GENETICS INC.

Query Match
                                                                                                                                                                                                                                                                                                       AAW23958 standard; protein; 353 AA. Mouse melatonin la receptor. W09803549-A1.
                                                                                                                                                                                                                                                                                                          Leceptor

J.98.
GEN HOSPITAL CORP.
6.4%;
Best Local Similarity 22.1%; Precedent 723
ID Mouse melatonin 1a // Precedent 723
PN US6326526-B1.
PD 04-DEC-200-7
PA (BRI'-200-7
PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2001.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , BRISTOL-MY.
Lery Match
Best Local Similarity 2
RESULT 724
ID AD029553 standa-
DE Mouse GPCR 7
PD 13-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 727
                                                                                                                                 Best_Local Similarity
RESULT 721
Best Local Similarity
RESULT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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ABP52133 standard; protein; 1025 AA.
Plasmodium falciparummultidrug resistance protein SEQ ID NO:85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-1992.

1 (MITU) MITSUBISHI KASEI CORP.

Query Match

Best Local Similarity 22.5%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vuciy match 6.4%; Score 77; DB 3; Length 1047; Best Local Similarity 20.4%; Pred. No. 34; RESULT 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 1202; 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 3; Length 1191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 991;
31;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 847;
25;
                                                                                                                                                                                                                                                                                                             DB 3; Length 805; 24;
                                                                                                                                                                                         DB 3; Length 728; 21;
                                                                     Length 690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG42380 standard; protein; 1191 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 52848.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG42379 standard; protein; 1202 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 52847.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A632547 standard; protein; 991 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 39285.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG42381 standard; protein; 1047 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 52849.
                                                                                                                       AAG42519 standard; protein; 728 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 53038.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                AAG32548 standard; protein; 847 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 39286.
EP1033405-A2.
06-SEP-2000.
AAG42520 standard; protein; 690 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 53039.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                              AGG35549 standard; protein; 805 AA. Arabidopsis thaliana protein fragment SEQ ID NO: 39287. EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%; Score 77; DB 5; 20.6%; Pred. No. 33;
                                                                        ٠<u>.</u>
                                                               DB 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 20.4%; Pred. No. RESULT 737
                                                                                                                                                                                           Score 77;
Pred. No. 2
                                                                        Score 77;
Pred. No.
                                                                                                                                                                                                                                                                                                                 6.4%; Score 77;
20.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.4%; Score 77; 20.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     6.4%; Score 77; 20.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR29527 standard; protein; 2510 AA.
AAR20527 standard; protein; 2510 AA.
EP518313-A2.
                                                                                                                                                                                                6.4%;
                                                                          6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 735
                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 733
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Best Local Similarity
RESULT 732
                                                                                         Best Local Similarity RESULT 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYGE-) UNIV GENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1217066-A1.
26-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1033405-A2.
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                                                                            Query Match
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Query Match
                                                                                                                                                                   ADC01137 standard; protein; 278 AA.
Enterchaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1181.
JP2002355074-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 6.4%; Score 76.5; DB 8; Length 481; Local Similarity 23.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.4%; Score 76.5; DB 2; Length 494; 21.3%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.4%; Score 76.5; DB 2; Length 494; 21.3%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-2002.
(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
ery Match 6.4%; Score 76.5; DB 6; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.4%; Score 76.5; DB 2; Length 509;
                                                                                                          Score 76.5; DB 8; Length 249;
Pred. No. 5.3;
                                                                                                                                                                                                                                                                           Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW20085 standard; protein; 509 AA.
Helicobacter pylori cytoplasmic protein, 10009666.aa
WO9640893-A1.
                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-2003.
(GENO-) GENOME THERAPEUTICS CORP.

Query Match
6.4%; Score 76.5; DB 7;

Best Local Similarity 21.8%; Pred. No. 12;
                                                                                                                                                                                                                                                                             DB 7;
                                                                                                                                                                                                                                                                                                                                        ABO65827 standard; protein; 435 AA.
Klebsiella pneumoniae polypeptide segid 12344.
US6610836-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW42996 standard; protein; 494 AA.
Putative mature potassium channel 2 protein.
US5710019-A.
                                                                                                                                                                                                                                                                           6.4%; Score 76.5; Di 28.5%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.4%; Score 76.5; I
21.3%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP58356 standard; protein; 494 AA.
Human potassium channel subunit Kv5.1.
WO200296944-A2.
ADF74966 standard; protein; 249 AA. Human 164-1h protein (SeqID 25). WOZO03097686-A1. CT-NOV-2003. (TAKE) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC99155 standard; protein; 494 AA.
Human mature K+ channel 2 protein.
US2003092895-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF74969 standard; protein; 481 AA.
Human 164-1b protein (SeqID 28).
WO2003097686-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR90765 standard; protein; 494 AA.
Human K+ channel 2 mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9603415-A1.
08-FEB-1996.
(HUMA-) HUMAN GENOME SCI INC.
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(HUMA-) HUMAN GENOME SCI INC.
                                                                                                              6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-2003.
(TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                  10-DEC-2002.
(UYTS-) UNIV TSUKUBA.
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Best Local Similarity
RESULT 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                         Best Local Similarity RESULT 740
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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(ADAM/) ADAMS M D.
(WHIT/) WHITE O R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D 19-DEC-1996.
A (ASTR ) ASTRA AB.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2003
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                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                       RESULT 741
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ABB08159 standard; protein; 570 AA.
Human cytoekeleton-associated protein (CSAP)-3 (ID: 7091536CD1)
                                                                                                                                                   G.4%; Score 76.5; DB 7; Length 555; Best Local Similarity 23.3%; Pred. No. 16; RESULT 749
                                                                                                                                                                                                                                                                                                                                          Length 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-WOV-2001.
(HUWA-) HUMAN GENOME SCI INC.
Lery Match 6.4%; Score 76; DB 5; Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA.) HUMAN GENOME SCI INC.

8ry Match

6.4%; Score 76; DB 3; Length 557;

3t Local Similarity 22.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUN46225 standard; protein; 615 AA.
Thermococcus kodakaraensis KOD1 protein sequence SeqID103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.4%; Score 76; DB 3; Length 274; 26.7%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%; Score 76; DB 3; Length 287; 26.7%; Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen protein sequence SEQ ID NO:940. W0200055351-A1. 21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 26.7%; Score 76; DB 3; Length RESULT 754

ID AAG05591 standard; protein; 287 AA.

PR Arabidopsis thaliana protein fragment SEQ ID NO: 7585.

PN PEP103405-A2.

PD 06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG09592 standard; protein; 274 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 7586.
EP1033405-A2.
GEP-2000.
                                                                                                                                                                                                                                                                                                                                       6.4%; Score 76.5; DB 5; 23.3%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                  AAW20918 standard; protein; 593 AA.
H. pylori transporter protein, 14gpl2015orf14
WO9640893-A1.
                                         ADB63857 standard; protein; 555 AA.
Human protein encoded by clone ASTR020053430.
EP1308459-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03
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Pred. No. 4.3;
Best Local Similarity 19.2%; Pred. No. 14; RESULT 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 76.5; 1
19.2%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.4%; Score 76.5; 22.6%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH88107 standard; protein; 195 AA.
Enterococcus faecalis polypeptide #2587.
US6617156-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-2004.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 26.7%; Fred. RESULT 755
ID ABB89424 standard; protein; 456 AA. DE Human polypeptide SEQ ID NO 1800. PN WO200190304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 557 AA
                                                                                                        07-MAY-2003.
(HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4%;
                                                                                                                                                                                                                                                                                            30-MAY-2002.
(INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOUC/) DOUCETTE-STAMM L A. (BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 756
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB53400 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1996.
(ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                             WO200242330-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-SEP-2003
                                                                                                                                                                                                                                                                                                                                          Query Match
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L-2001.

AAA ) PHARMACIA & LOCAL SIMILATITY ABESULT 768
ID AD029507 standar DN W020040.

PD 13.
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RESULT 775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
RESULT 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB15936 standard; protein; 352 AA.
E. coli proliferation associated protein sequence SEQ ID NO:293
WO200044906-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU02182 standard; protein; 276 AA.
S. pneumoniae type 4 strain protein from coding region #1759.
WO200277021-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 75.5; DB 7; Length 363; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75.5; DB 3; Length 352;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 264;
                                                                                                                                                                                                                                   Score 75.5; DB 4; Length 228; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 8; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 342
                                                                                                                                                                                                                                                                                                                                                                    Length 263;
                                                                                                     Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. albicans BAX-associated protein fragment SEQ ID 528 WO200264766-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY81619 standard; protein; 264 AA.
Streptococcus pneumoniae type 4 protein sequence #119
WO200006737-A2.
                                                                                                                                                    ABB63150 standard; protein; 228 AA.
Drosophila melanogaster polypeptide SEQ ID NO 16242.
Drosophila melanogaster polypeptide SEQ ID NO 16242.
27-282-2001.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                   ADK46633 standard; protein; 263 AA.
Streptococcus pneumoniae protein, Seg ID No 3148.
US6699703-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                    ADM92206 standard; protein; 263 AA.
S pneumoniae antigenic protein sequence SeqID403
WO2004020609-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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ry Match
6.3%; Score 75.5; DB 3;
t Local Similarity 18.0%; Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH51470 standard; protein; 363 AA.
Rat MT1 receptor amino acid sequence #SEQ ID 2.
FR2835847-A1.
                                                                   (DUPO ) DU PONT DE NEMOURS & CO E I.
(DUPO ) DU PONT DE NEMOURS & CO E I.
ery Match
(Fr. Score 76; DB 3;
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                                                                                                                                                                                                                                                                                                                                                                Score 75.5; DB
Pred. No. 7.5;
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18.0%; Pred. No. 7.5;
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 75.5;
Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG93285 standard; protein; 342 AA
                  AAY44945 standard; protein; 593 AA.
Wheat sulphate permease-2.
WO200004154-A2.
                                                                                                                                                                                                                                                                                                                                 02-MAR-2004.
(GENO-) GENOME THERAPEUTICS CORP.
(ery Match
ery Match similarity 18.0%; Prec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-AUG-2003.
15-AUG-2003.
(SERV-) LES LAB SERVIER SA.
6.3%;
dery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3%;
                                                                                                                                                                                                                                      6.3%;
21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2002.
(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 764
                                                                                                                   Best Local Similarity RESULT 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
RESULT 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAR-2004.
(TUFT ) UNIV TUFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                  Best Local Similarity RESULT 759
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
      RESULT 757
ID AAY449
DE Wheat
PN WO2000
PD 27-JAN
PA (DUPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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AAU03852 standard; protein; 433 AA.
G protein-coupled receptor-like (GPCR-like) receptor protein #24.
G protein-coupled receptor-like (GPCR-like) receptor protein #24.
31-MAY-2001.
(PHAA ) PHARMACIA & UPJOHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU03820 standard; protein; 499 AA.
G protein-coupled receptor-like (GPCR-like) receptor protein #19.
WO200138533-A2.
AAU03851 standard; protein; 397 AA.
G protein-coupled receptor-like (GPCR-like) receptor protein #23.
WO200138533-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -A-M-2436 standard; protein; 445 AA.
Propionibacterium acnes predicted ORF-encoded polypeptide #7112.
WO2003033515-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP99138 standard, protein, 480 AA.
Human transporter and ion channel (TRICH) protein - SEQ ID 3.
WO2004048599-A2.
                                                                                                                                                                                                                                           DB 4; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                       Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 499
                                                                                          DB 4; Length 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 445;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 75; DB 8; Length 392; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3%; Score 75; DB 4; Length 445; 24.8%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes immunogenic protein #6813.
W0200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                       Score 75.5; DB 8;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENO-) GENOME THERAPEUTICS CORP.

(GENO-) GENOME THERAPEUTICS CORP.

6.3%; SCORE 75; DB 6;

ery_Match

23.1%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.3%; Score 75; DB 8; 21.0%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM72132 standard; protein; 392 AA.
Human NTRAN polypeptide (clone ID 7524555CD1).
WO2004022705-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 75.5; I
Pred. No. 18;
                                                                                                                                                                                                                                         Score 75.5;
Pred. No. 15;
                                                                                          Score 75.5; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.3%; Score 75; 24.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA34178 standard; protein; 467 AA. Acinetobacter baumannii protein #1339.
                                                                                                                                                                                                                                                                                                 ADO29507 standard; protein; 471 AA. Mouse GPCR HTR2A, SEQ ID NO:609.
                                                                                                                                                                                                                                                                                                                                                                                           6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3%;
                                                    MAX-2001.
(PHAA ) PHARMACIA & UPJOHN.
(ery Match 6.3%;
                                                                                                                                                                                                                                              6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-2001.
(PHAA ) PHARMACIA & UPJOHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-2004.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2003.
(CORI-) CORIXA CORP.
                                                                                              Query Match
Best Local Similarity
RESULT 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 773
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Best Local Similarity
RESULT 770
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Best Local Similarity
RESULT 771
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Best Local Similarity
RESULT 772
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Best Local Similarity
RESULT 769
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(ICOS-) ICOS CORP.

Query Match

POSED

Query Match

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PD 20-APR-2000...
PA (AREN-) ARENA PHARM INC.
Query Match
Best Local Similarity 25.8%; Pred. No. 15;
RESULT 786
                     6.2%; Score 74.5; DB 2; Length 355;
25.8%; Pred. No. 15;
                                                                                                                                                              DB 2; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%; Score 74.5; DB 3; Length 355; 25.8%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.2%; Score 74.5; DB 4; Length 355; 25.8%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 355,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 355
                                                                                                                                                                                                              AAY90677 standard; protein; 355 AA.
Human mutant G protein-coupled receptor V28 (1230K)
WO200022129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB21693 standard; protein; 355 AA.
Human 7TM receptor V28 cDNA clone protein #2.
US6107475-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 355 AA.
V28 cDNA clone protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A4091235 standard; protein; 355 AA.
Human 7 transmembrane domain receptor V28 #2.
US6348574-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU91234 standard; protein; 355 AA.
Human 7 transmembrane domain receptor V28 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2%; Score 74.5; I
25.8%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 74.5; I
Pred. No. 15;
                                                                                                                                                           Score 74.5; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.2%; Score 74.5;
25.8%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 74.5;
Pred. No. 15;
                                                                     AAV48722 standard; protein; 355 AA.
Human V28 seven transmembrane receptor.
US5759804-A.
                                                                                                                                                                                                                                                                                                                                              Human G protein-coupled receptor V28. WO200022129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG80126 standard; protein; 355 AA.
Human CX3CR1 protein.
WO200172830-A2.
04-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB82786 standard; protein; 355 AA.
Human CX3C chemokine receptor 1.
WO200150406-A1.
23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                  WOZOWCZ-
20-APR-2000.
(AREN-) ARENA PHARM INC.
G-2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC. (NOUN ) UNIV NORTHWESTERN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%;
25.8%;
                                                                                                                                                            6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IPFP-) IPF PHARM GMBH. (FORS/) FORSSMANN U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 792
                    Query Match
Best Local Similarity
RESULT 784
                                                                                                                                                            Query Match
Best Local Similarity
RESULT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 7TM receptor
US6107475-A.
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RESULT 789
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RESULT 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB21692 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D 22-AUG-2000.
A (ICOS-) ICOS CORP.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-2002.
(ICOS-) ICOS CORP.
                                                                                                                          02-JUN-1998.
(ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-2000.
(ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6348574-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB66797 standard; protein; 200 AA.
Portine reproductive and respiratory syndrome virus ORF #5 protein.
WO200102858-A1.
11-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.2%; Score 74.5; DB 4; Length 200; 23.8%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7; Length 1131; 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.3%; Score 75; DB 4; Length 2248; 22.9%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1051;
                                                                                                                                                                                                                                                                                                                                                                                                                            6.3%; Score 75; DB 2; Length 1051; 23.4%; Pred. No. 59;
                                                                                                    Score 75; DB 7; Length 549;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG20763 standard; protein; 2248 AA.
Drosophila melanogaster rutabaga protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB64494 standard; protein; 2248 AA.
Drosophila melanogaster polypeptide SEQ ID NO 20274.
WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%; Score 74.5; DB 8; 23.3%; Pred. No. 9.5;
                                                                                                                                                                                                              24-MAY-1994.
(TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
(SANW ) SANWA KAGAKU KENKYUSHO CO.
(TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                       6.3%; Score 75; DB 2; 23.4%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Auroa 12 Standard; protein; 1131 AA.
Human protein encoded by clone NT2NE20077270.
EP1308459-A2.
                                                                                                                                              AAR54066 standard; protein; 1051 AA.
Non-A, non-B hepatitis virus gene #4 product.
JP06141870-A.
                                                                                                                                                                                                                                                                                                                                        AAR98361 standard; protein; 1051 AA.
5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).
JP07133291-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.3%; Score 75;
Best Local Similarity 23.9%; Pred. No. (RESULT 779
ADH86490 standard; protein; 549 AA.
Enterococcus faecalis polypeptide #970.
US6617156-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) INST MOLECULAR AGROBIOLOGY. (MATE-) INST MATERIALS RES & ENG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR53748 standard; protein; 355 AA.
Seven transmembrane receptor (V28).
W09412635-A2.
09-JUN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADF74954 standard; protein; 256 AA. Rat 164-1h protein (SeqID 13). WO2003097686-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-2003.
(HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                           6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD.
                                                      09-SEP-2003.
(DOUC/) DOUCETTE-STAMM L A.
(BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1995.
(TOFU ) TONEN CORP.
                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-2003
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Query Match

RESULT 782

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Query Match
Best Local Similarity
RESULT 805
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             US2003105292-A1.
05-UUN-2003.
(LIAW/) LIAW C W.
(BEHA/) BEHAN D P.
(CHAL/) CHALMERS D T
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 804
                                                                                                                                                                                                                             Best Local Similarity RESULT 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 807
Human serotonin V28.
                                                                                                                                                                                                                                                                                                             13-MAY-2004.
(PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-SEP-1998
                                                                                                                                                                                       18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP81882 standard; protein; 355 AA. Human CX3C chemokine fractalkine receptor 1 protein SEQ ID NO:249. WO200261087-A2.
                                                                                 AAU84327 standard; protein; 355 AA.
Protein CX3CR1 differentially expressed in breast cancer tissue.
W0200210436-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 74.5; DB 7; Length 355;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 355
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 355,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 355
                                                                                                                                                                           Length 355;
                                                                                                                                                                                                                                                                                                      Length 355;
                                    Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC22649 standard; protein; 355 AA.
Human G protein-coupled receptor (GPCR) polypeptide #34
US6555339-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC22751 standard; protein; 355 AA.
Human G protein-coupled receptor (GPCR) polypeptide #74
US6555339-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP97732 standard; protein; 355 AA.
Amino acid sequence of human chemokine receptor CX3CR1.
WO2003014153-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 74.5; DB 7; 25.8%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7;
                                                                                                                                                                                                                                                                                                   6.2%; Score 74.5; DB 6; 25.8%; Pred. No. 15;
                                     DB 5;
                                                                                                                                                                               2,
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                               В
                                                                                                                                                                                                                           ABRS6524 standard; protein; 355 AA.

Human chemokine (C-X3-C) receptor 1 protein.
WO2003025138-A2.
27-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74.5; 1
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.2%; Score 74.5; 25.8%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 74.5; i
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%; Score 74.5; 1
25.8%; Pred. No. 15;
                                       Score 74.5; 1
Pred. No. 15;
                                                                                                                                                                             6.2%; Score 74.5; 25.8%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                  AAO29513 standard; protein; 355 AA.
Human fractalkine receptor (313) protein.
WO2003039475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADMI4224 standard; protein; 355 AA. Mutated human serotonin V28. US2003105292-A1. 05-UV-2003. (LIAW/) LIAW C W. (BEHA/) BEHAN D P. (CHAL/) CHALMERS D T.
                                                                                                                                   07-FEB-2002.
(BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
(BAAK/) BAAK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH14122 standard; protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-2002.
(LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Je humar.

Jery Match
Best Local Similarity 25.8%; Pre-
RESULT 797
ID ABP81882 standard; prof-
PR WO200261087
PD WO200261087
PD 08-AIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.2%;
                                                                                                                                                                                                                                                                                         (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2003.
(MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.2%;
Best Local Similarity 25.8%;
RESULT 798
                                        6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-APR-2003.
(AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMENA PHARM
Local Similarity
RESULT 799
ID ADC22649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 801
                                                                                                                                                                             Ouery Match
Best Local Similarity
RESULT 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 795
                                          Query Match
Best Local Similarity
RESULT 793
             19-FEB-2002.
(ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Si
RESULT 796
                                                                                                                                                                                                                                                                                                           Query Match
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Score 74.5; DB 2; Length 471;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 74.5; DB 2; Length 471;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 471;
                                                                                                                               Score 74.5; DB 8; Length 355;
Pred. No. 15;
                                                                                                                                                                                                                                                                          DB 8; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 355
 DB 7; Length 355;
                                                                                                                                                                                                                                                                                                                         ADQ18141 standard; protein; 355 AA.
Human soft tissue sarcoma-upregulated protein - SEQ ID
WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.2%; Score 74.5; DB 2;
21.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW77110 standard; protein; 471 AA.
Rat 5-HT2A serotonin receptor C322R mutant.
WO9838217-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW77111 standard; protein; 471 AA.
Rat 5-HT2A serotonin receptor C322E mutant.
WO9838217-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 74.5; 1
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WACON-2004.

(PROT-) PROTEIN DESIGN LABS INC.

(PROT-) PROTEIN DESIGN LABS INC.

6.2%; Score 74.5; 1

6ry Match

7.3.1 similarity 25.8%; Pred. No. 15;
Query Match 6.2%; Score 74.5; I Best Local Similarity 25.8%; Pred. No. 15; RESULT 802
                                                                                                                                                                                                                                                                            6.2%; Score 74.5; 1
25.8%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW77104 standard; protein; 471 AA
                                                      ADHIOGEO standard; protein; 355 AA.
Human CX3CR1 polypeptide.
WO2003104484-A1.
                                                                                                                                                                                         AD029269 standard; protein; 355 AA.
Human GPCR CX3CR1, SEQ ID NO:370.
W02004040000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat 5-HT2A serotonin receptor WO9838217-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%;
                                                                                                                                        6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TEIT/) TEITLER M.
(HERR/) HERRICK-DAVIS K.
(EGAN/) EGAN C C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TEIT/) TEITLER M.
(HERR/) HERRICK-DAVIS K.
(EGAN/) EGAN C C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-1998.
(TEIT/) TEITLER M.
(HERR/) HERRICK-DAVIS K.
(EGAN/) EGAN C C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TEIT/) TEITLER M. (HERR/) HERRICK-DAVIS K. (EGAN/) EGAN C C.
                                                                                                                            (META-) METABOLEX INC
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6.2%; Score 74.5; DB 5; Length 3010; 23.8%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1808;
                                                                          Query Match 6.2%; Score 74.5; DB 5; Length 471; Best Local Similarity 21.0%; Pred. No. 22; RESULT 810
                                                                                                                                                                                                                                                                                                                                                       O 65-SEP-2001.

A (HELI-) HELIX RES INST.

Guery Match

6.2%; Score 74.5; DB 4; Length 562;

Best Local Similarity 23.1%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL31569 standard; protein; 562 AA.
Human protein encoded by a full length cDNA clone SeqID 3602
EP1396543-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%; Score 74.5; DB 8; Length 562; 23.1%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2%; Score 74.5; DB 4; Length 597; 27.2%; Pred. No. 31;
                                                                                                                                                                                                                                             DB 8; Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 74; DB 7; Length 154;
Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB62948 standard; protein; 597 AA.
Drosophila melanogaster polypeptide SEQ ID NO 15636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 74.5; DB 5; 17.3%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB92731 standard; protein; 1808 AA.
Herbicidally active polypeptide SEQ ID NO 1942.
WO200210210-A2.
                                                                                                                                                                                                                                             6.2%; Score 74.5; 1
23.3%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.2%; Score 74.5; 321.1%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADAJ6878 standard; protein; 940 AA.
Acinetobacter baumannii protein #4039.
US6562958-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2002.
(MOLE-) INST MOLECULAR & CELL BIOLOGY.
(EHRL/) EHRLICH G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE20477 standard; protein; 3010 AA.
HCV-S1 full-length polyprotein.
WO200208447-A2.
                                                                                                                                                                                                                                                                                            AAM93692 standard; protein; 562 AA.
Human polypeptide, SEQ ID NO: 3602.
EP1130094-A2.
ABB07980 standard; protein; 471 AA.
Rat 5-HT2 receptor sequence.
US6383762-B1.
                                                                                                                                                ADF74971 standard; protein; 481 AA. Rat 164-1b protein (SeqID 30). WO2003097686-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF07294 standard; protein; 154 AA.
Bacterial polypeptide #3407.
US6605709-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAY-2003.
(GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-2003.
(GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%;
                                                      07-MAY-2002.
(SYNA-) SYNAPTIC PHARM CORP.
                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2.
27-SEP-2001.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                           Best Local Similarity RESULT 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2002.
(FARB ) BAYER AG.
                                                                                                                                                                                                          27-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 816
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
                                                                                                                                                                                                                                                                                                      PPREE
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cuery Match INST GENOMIC RES.

Cuery Match (6.2%; Score 74; DB 6; Length 324; BESULT 822

ID AB000448 standard; protein; 342 AA.

PDE Novel human polypeptide #35.

PD 20-MR-2003

PD 20-MR-2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU02869 standard; protein; 324 AA.
S. pneumoniae type 4 strain protein from coding region #2450.
WO200277021-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 18.5%; Pred. No. 17; Length 350; RESULT 827
                                                                                              DB 6; Length 231;
                                                                                                                                                                                                                                                 6; Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.2%; Score 74; DB 6; Length 342; 21.2%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%; Score 74; DB 2; Length 350; 18.5%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP81840 standard; protein; 350 AA. Human melatonin receptor type la protein SEQ ID NO:164. WO200261087-A2.
ABU70365 standard; protein; 231 AA.
Human adipocyte bait protein, melatonin receptor_V4.
WO200286122-A2.
                                                                                                                                                 ABU70366 standard; protein; 231 AA.
Human adipocyte bait protein, melatonin receptor_VS.
W0200286122-A2.
31-OCT-2002.
(HYBR-) HYBRIGENICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 31-MAR-1997.

PA (TAKE) TAKEDA CHEM IND LTD.

QUETY MATCh 6.2%; Score 74; DB 2;

Best Local Similarity 18.5%; Pred. No. 17;

RESULT 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.2%; Score 74; DB 2; Best Local Similarity 18.5%; Pred. No. 17; RESULT 826
                                                                                                                                                                                                                                                                                                                                                       6.2%; Score 74; DB 6 18.5%; Pred. No. 9.4;
                                                                                            6.2%; Score 74; DB (18.5%; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW94761 standard; protein; 350 AA.
Human melatonin receptor protein mel-la.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR88412 standard; protein; 350 AA. High-affinity melatonin-la receptor. WO9535320-A1.
                                                                                                                                                                                                                                                                                        ABB54180 standard; protein; 312 AA.
Lactococcus lactis protein yilG.
FR2807446-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-DEC-1995. (MASS-) MASSACHUSETTS GEN HOSPITAL. 6.2%; Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMM15786 standard; protein; 350 AA. Melatonin receptor protein. JP09084581-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-AUG-2002.
(LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JAN-1999.
(JCRP-) JCR PHARM CO LID.
                                                      31-OCT-2002.
(HYBR-) HYBRIGENICS.
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 821
                                                                                                Best Local Similarity
RESULT 819
                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP892046-A2.
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                              Query Match
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Lory Match
Best Local Similarity
RESULT 845
ID AAB86544
DE ''
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
RESULT 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2001.
(KERN/) KERN F.
                                                                                                                                                                                                                                                                                                                                   06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73.5; DB 3; Length 120;
Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%; Score 74; DB 2; Length 1031; 26.2%; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 74; DB 2; Length 1031; 26.2%; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 74; DB 6; Length 366;
21.8%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%; Score 74; DB 4; Length 493; 22.5%; Pred. No. 27;
                                                                                                                                                                                                                                Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2001.
1 (INRG) INRA INST NAT RECH AGRONOMIQUE.
QUERY MATCH
6.2%; SCOIE 74; DB 5; Length 442;
Best Local Similarity 20.4%; Pred. No. 23;
                                                                                  Score 74; DB 8; Length 350;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY80509 standard; protein; 492 AA.
F. lutescens L-lysine:2-oxoglutarate 6-aminotransferase.
WO200008170-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG59839 standard; protein; 120 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 77442.
EP1033400-A2.
06-8EP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG64105 standard; protein; 493 AA.
Flavobacterium lutescens L-lysine-6-aminotransferase
WC200148216-A1.
05-JUL-2001.
                                                                                                                                      AAW19220 standard, protein; 364 AA.
Rat growth hormone secretagogue receptor type Ia.
W09721730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-1994.
(TOKR.) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
(TOKR.) ZH TOKYOTO RINSHO IGAKU CO.
(TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%; Score 74; DB 3; 22.5%; Pred. No. 27;
                                                                                                                                                                                                      19-JUN-1997.

(MERI ) MERCK & CO INC.

6.2%; Score 74; DB 2;

177 Match

19.4%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AARS4067 standard; protein; 1031 AA.
Non-A, non-B hepatitis virus gene #6 product
JP06141870-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR98362 standard; protein; 1031 AA. 5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#6). JP07133291-A.
                                                                                                                                                                                                                                                                                    ABM73179 standard; protein; 366 AA. Staphylococcus aureus protein #2419 WO200294868-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              ABB55224 standard; protein; 442 AA.
Lactococcus lactis protein yteD.
FR2807446-Al.
ADO29552 standard; protein; 350 AA.
Human GPCR MTRRIA, SEQ ID NO:654.
MO2004040000-A2.
13-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.2%;
                                                                                         6.2%;
                                                                                                                                                                                                                                                                                                                an.

2002.

2002.

LR) CHIRON SPA.

LTY Match

Best Local Similarity 2.

RESULT 830

ID ABB55224 standaring DE Lactococcur

PN FR28074.

PD 12-6

PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-2000.
(SAOC ) MERCIAN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SAOC ) MERCIAN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 834
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TOFU ) TONEN CORP.
                                                                        (PRIM-) PRIMAL INC.
Query Match
                                                                                                        Local Similarity
                                                                                                                                                                                                    19-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 831
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6.2%; Score 73.5; DB 4; Length 491; 19.3%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 442;
AAU25578 standard; protein; 192 AA.

Human G Protein-Coupled Receptor (GPCR) polypeptide #25.

N 00200162797-A2.
30-AMG-2001.
A CHAAA ) PHARMACIA & UPJOHN CO.
Query Match
Best Local Similarity 26.3%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                      Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG51384 standard, protein; 489 AA.
Arabiogopsis thaliana protein fragment SEQ ID NO: 65210.
BP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGS1385 standard; protein; 442 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 65211.
BP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG32486 standard; protein; 442 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 39198.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG32487 standard; protein; 377 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 39199.
BP1033405-A2.
66-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGS1386 standard; protein; 377 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 65212.
EPI033405-A2.
66-SEP-2000.
                                                                                                                                                                                                                                                                                                                                       AGG32488 standard; protein; 282 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 39200.
EP1033405-A2.
                                                                                                                                                                           ABU44044 standard; protein; 268 AA.
Protein encoded by Prokaryotic essential gene #29571
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.2%; Score 73.5; DB 3; 28.1%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%; Score 73.5; DB 3; 28.1%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AABB6544 standard; protein; 491 AA.
Human cytomegalovirus strain AD169 IB1 protein.
WO200163286-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.2%; Score 73.5; 1
28.1%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73.5; Pred. No. 30;
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 19.6%; Pred. No. 13;
RESULT 838
                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 73.5; C
28.1%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEOO.) GENOME THERAPEUTICS CORP.

ry Match
6.2%; Score 73.5; C
t. Local Similarity 17.4%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2%; Score 73.5; I
28.1%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADF05982 standard; protein; 312 AA. Bacterial polypeptide #2095. US6605709-B1. 12-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%;
                                                                                                                                                                                                                                                    03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
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Length 1287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3033;
                                                                                                                                                                                                                              Length 491;
                                                                                                                                                                                                                                                                                                                                                               Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 574;
                                                                                                Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73; DB 2; Length 114;
Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaëter polypeptide SEQ ID NO 12003.
WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 114 AA.
or periplasmic protein 80257.aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP73574 standard; protein; 574 AA.
Candida albicans essential protein SEQ ID NO 7411.
WO200253728-A2.
                                                                                                                                                                                                                                                                                                                      21-MAX-2004.
(EXPR-) EXPRESSION DIAGNOSTICS INC.
(eXPR-) EXPRESSION DIAGNOSTICS INC.
6.2%; Score 73.5; DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAY-2004.

(EXPR-) EXPRESSION DIAGNOSTICS INC.

Query March

6.2%; Score 73.5; DB 8;

Best Local Similarity 19.3%; Pred. No. 31;
                                                                                                DB 8;
                                                                                                                                                                                                                               DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.2%; Score 73.5; DB 4; 18.2%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 73.5; DB 2;
Pred. No. 3.8e+02;
               ADP12517 standard; protein; 491 AA.
Protein encoded by mRNA of the invention #127.
21-MAY-2004.
                                                                                                                                            ADP12518 standard; protein; 491 AA.
Protein encoded by mRNA of the invention #128.
WO2004042346-A2.
                                                                                                                                                                                                                                                                             ADP12513 standard; protein; 491 AA.
Protein encoded by mRNA of the invention #123
WO2004042346-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            ADP12514 standard; protein; 491 AA.
Protein encoded by mRNA of the invention #124
WO2004042346-A2.
                                                                                                                                                                                       M.V. 21-MAY.2004.

(EXPR-) EXPRESSION DIAGNOSTICS INC.

(EXPR-) EXPRESSION DIAGNOSTICS INC.

6.2%; Score 73.5; D

6.1%; Pred. No. 31;
                                                                            (EXPR.) EXPRESSION DIAGNOSTICS INC.

12 Match

12 Local Similarity 19.3%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.2%; Score 73.5; 1
20.8%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 73.5; 1
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG29128 standard; protein; 682 AA.
Novel human diagnostic protein #29119.
MO200175067-A2.
11-OCT-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR33214 standard; protein; 3033 AA.
NANBH virus strain HC-J8 protein.
EP532167-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB61737 standard; protein; 1287 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.1%;
21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-1993.
A (IRMO) IMMUNO JAPAN INC.
Query Match
Best Local Similarity 27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2002.
(ELIT-) ELITRA PHARM INC.
                                     J46-A2.

2004.

LYN MITCH
BEST LOCAL SIMILARITY
RESULT 847
ID ADP12518 stand-
DE Protein err
PN W020040
PP 21-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD 19-DEC-1996.
PA (ASTR ) ASTRA AB.
Query Match
Best Local Similarity
RESULT 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW20571 standard;
H. pylori secreted
WO9640893-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Si
RESULT 851
                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                Query Match
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Best Loc.
RESULT 853
ID AAR337
DE NANPY
PN EPF
PD J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 852
ID ABB617
DE Drosop
PN WO2001
PD 27-SEP
PA (PEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 850
ID ABP735
DE Candid
PN WO2002
PD 11-JUL
PA (ELIT-
RESULT 846
ID ADP125
DE Protei
PN WO2004
PD 21-MAY
PA (EXPR-
                                                                                                                                                                                                                                                                RESULT 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
RESULT 854
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DB 5; Length 189;
                                                                                                                                                                                                                             Length 199;
                                                                                                                                                                                                                                                                                                                                                                                      Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%; Score 73; DB 5; Length 272; 19.9%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.1%; Score 73; DB 8; Length 272; 19.9%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%; Score 73; DB 6; Length 290; 23.4%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.1%; Score 73; DB 6; Length 322; 20.6%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR47464 standard; protein; 322 AA.
Breast cancer associated protein sequence SEQ ID NO:160.
WO2003004989-A2.
16-JAN-2003.
ID AAU69567 standard; protein; 189 AA.

BE Human G protein-coupled receptor from cDNA Seq-2643.

PN W0200177330-A2.

PD 18-OCT-2001.

PA (PHAA) PHARMACIA & UPJOHN CO.

QUETY Match

Best Local Similarity 20.3%; Pred. No. 9.3; Lengt RESULT 856
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU87836 standard; protein; 272 AA.
T. aureum 7091 elongase TELO1 from plasmid pRAT-4-Al
WO200208401-A2.
                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.1%; Score 73; DB 5; Beet Local Similarity 24.6%; Pred. No. 14; RESULT 858
                                                                                                                                                                                                                             6.1%; Score 73; DB 7; 22.6%; Pred. No. 10;
                                                                                                                                                                                                                                                                                ABP29367 standard; protein; 249 AA.
Streptococcus polypeptide SEQ ID NO 7910.
WO200234771-A2.
                                                                                                                                        ADC97146 standard; protein; 199 AA.
E faecium protein sequence SEQ ID 6773.
US6583275-B1.
24-UUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH80191 standard; protein; 272 AA.
Fungal 7091 elongase protein seq id 75.
US2003163845-Al.
28-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM73154 standard; protein; 290 AA. Staphylococcus aureus protein #2394.WO200294868-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN61865 standard; protein; 349 AA.
Human novel protein NOV42a.
US2004043382-A1.
                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A (MILL-) MILLENIUM PHARM INC.
Query Match
Best Local Similarity 20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MUKE/) MUKERJI P.
(LEON/) EUN-YEONG LEONARD A.
(HUAN/) HUANG Y.
(PERE/) PEREIRA S L.
                                                                                                                                                                                                                                                                                                                                02-MAY-2002.
(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZERHUSEN B D.
GUSEV V Y.
JI W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PADIGARU M.
SPYTEK K A.
SHENOY S G.
TAUPIER R J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2002.
(ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 861
                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENA C E A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SPYT/)
(SHEN/)
(TAUP/)
(PENA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZERH/)
(GUSE/)
(JIWW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PADI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 862
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06-SEP-2000.
                                                                                                                                                                                                      03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB97377 standard; protein; 364 AA.
Rat growth hormone secretagogue receptor (GHSR) related protein.
WO200132705-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 415; 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.1%; Score 73; DB 8; Length 364; 19.4%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 364; 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.1%; Score 73; DB 3; Length 364; Best Local Similarity 19.4%; Pred. No. 23; RESULT 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.1%; Score 73; DB 4; Length 364;
19.4%; Pred. No. 23;
                                                                                                                                                                                                                                                                      6.1%; Score 73; DB 8; Length 349; 24.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG50065 standard, protein, 415 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 63404.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW77773 standard; protein; 377 AA.
Staphylococcus aureus protein of unknown function.
EP841394-A2.
13-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK.) SMITHKLINE BEECHAM CORP.
(SMIK.) SMITHKLINE BEECHAM PLC.
5.17 Match
6.1%; Score 73; DB 2;
1. Local Similarity 23.3%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                           AAW19613 standard; protein; 364 AA.
AAW19613 standard; protein; 364 AA.
W09722004-A1.
                                                                                                                                                                                                                                                                                                                                                                                                             AAY54565 standard; protein; 364 AA.
Anuse growth hormone secretagogue receptor.
WO200002918-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                           Score 73;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO29026 standard; protein; 364 AA. Mouse novel GPCR GHSR, SEQ ID NO:125. WO2004040000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1%;
                                                                                                                                                                                                                                                                                                                                                                            6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-2001.
(TAKE ) TAKEDA CHEM IND LID.
                                                                                                                                                                                                                                                                                                                                                                (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JAN-2000.
(MERI ) MERCK & CO INC.
                                                                                                                                                 LIUY.
ANDERSON D W.
SPADERNA S K.
CATTERTON E.
LIBITE M W.
ALSOBROOK J P.
LEDLEY D M.
ALEGER D K.
RIEGER D K.
RIEGER D K.
                                                                                                                                                                                                                                                                                                                                 L997.
L971.
L971.
Lery Match
Best Local Similarity 1>
RESULT 864
ID AAY54565 stander
DE A mouse grow
PN W02000°
PP 20-
                                                                                                 FERNANDES E R.
CASMAN S J.
MALYANKAR U M.
GERLACH V.
                                  PATTURAJAN M.
GANGOLLI E A.
VERNET C A M.
GUO X S.
TCHERNEV V T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 867
                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 866
GORMAN L.
MILLER C E.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAY-2004.
(PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                              Query Match
                                                                                                     (FERN/)
(CASM/)
                                                                            (GUOX/)
                                                  (GANG/)
                                                                                                                                                                  ANDE/)
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RESULT 868
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6.1%; Score 73; DB 2; Length 495; 23.2%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%; Score 73; DB 3; Length 472;
19.8%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                              GELTT-) ELITRA PHARM INC.
(ELIT-) ELITRA PHARM INC.
(**14) MATCh
(**14) MATCh
(**14) Local Similarity 26.5%; Pred. No. 31;
                                                                                                                                                                                                Length 430;
                                                                         Length 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGS50063 standard; protein; 474 AA.
AAGS0063 standard; protein fragment SEQ ID NO: 63402.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                            AGG50064 standard; protein; 472 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 63403.
BE1033405-A2.
06-SEP-2000.
                                                                                                                      AAG24012 standard; protein; 430 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 27527.
BP1033405-A2.
06-SEP-2000.
AAG24013 standard; protein; 427 AA.
Arabidopeis thaliana protein fragment SEQ ID NO: 27528.
EP1033405-A2.
                                                                                                                                                                                                                                           ABU31419 standard; protein; 453 AA.
Protein encoded by Prokaryotic essential gene #16946.
W0200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE ABM70313 standard; protein; 490 AA.

DE Photorhabdus luminescens protein sequence #3410.

PN W0200294867-A2.

PD 28-NOV-2002.

PA (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.

Query Match

Best Local Similarity 24.6%; Pred. No. 35;

RESULT 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73; DB 7;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 73; DB 5;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%; Score 73; DB 3;
19.8%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY33766 standard; protein; 495 AA.
hkv5.1 human brain-specific potassium channel.
WO9941372-A1.
                                                                           DB 3;
29;
                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klebsiella pneumoniae polypeptide segid 9817.
US6610836-B1.
                                                                                                                                                                                                     DB 29;
                                                                                                                                                                                                     Score 73;
Pred. No. 2
                                                                               Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP53583 standard; protein; 526 AA.
Human NOV13b protein SEQ ID NO:30.
WO200262999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH42229 standard; protein; 526 AA.
Novel human protein NOV50d.
WO2003102159-A2.
11-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-2003.
(GENO-) GENOME THERAPEUTICS CORP.
GENO-) GENOME THERAPEUTICS SCOFF
ery Match (18, SCOFF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 6.1%;
Local Similarity 23.3%;
                                                                                                                                                                                                         6.1%;
                                                                               6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 876
ID ABO63300 standard; px
DE Klebsiella pneumoniae
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-1999.
(ZENE ) ZENECA LTD.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 873
                                                                           Query Match
Best Local Similarity
RESULT 870
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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6; Length 792;

us-10-063-518-14.rag.spdi

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ABJ19057 standard; protein; 792 AA.
Pathogen specific antigen related staphylococcal protein SEQ ID No 334.
WO200259148-A2.
                                                                                                                                                                                                                                                                                                                                              AAW68466 standard; protein; 845 AA.
Protein encoded by fragment #6 isolated from Hepatitis C virus genome.
WO9825960-A1.
                                                                                                                                                                                                                                                                                       Score 73; DB 6; Length 792;
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 913;
83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.1%; Score 73; DB 8; Length 966; 11.3%; Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%; Score 73; DB 4; Length 971; 19.5%; Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1%; Score 73; DB 4; Length 976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ76159 standard; protein; 966 AA.
Marker gene related amino acid sequence SEQ ID NO:1411.
EP1394274-A2.
                                                                                                                                                                                                                                                                                                                                                                                                PA (CURT) CURTIS R A J.

PA (SILO/) SILOS-SANTIAGO I.

Query Match

Best Local Similarity 21.3%; Pred. No. 90;

RESULT 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 18-OCT-2001.

PA (MILL-) MILLENIUM PHARM INC.

Query Match

Best Local Similarity 21.3%; Pred. No. 90;
                                                                                             PD 01-AUG-2002.

PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

Query Match 6.1%; Score 73; DB
BBE Local Similarity 23.3%; Pred. No. 68;

RESULT 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM51861 standard; protein; 966 AA.
Murine polycystic kidney disease protein 2.
WO200177331-A1.
 23.3%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB07819 standard; protein; 966 AA.
Mouse polycystic kidney disease protein 2.
US2002035056-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.1%; Score 73;
19.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG24246 standard; protein; 913 AA.
Novel human diagnostic protein #24237.
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG05866 standard; protein; 971 AA. Novel human diagnostic protein #5857. WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG07373 standard; protein; 976 AA. Novel human diagnostic protein #7364. W0200175067-A2.
                                                                                                                                                                                     Stabhylococcus aureus protein, 792 AA. Staphylococcus aureus protein #2357. AV. 000294868-A2. SB-NOV-2002. (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                         6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 03-MAR-2004.
1 (GENO-) GENOX RES INC.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 895
Best Local Similarity
RESULT 888
                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 890
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2001.
(HYSE-) HYSEQ INC.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU37199 standard; protein; 748 AA.
Staphylococcus aureus cellular proliferation protein #1369
WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) 27-SEP-2001.
1 (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 4; Length 792;
                     Score 73; DB 8; Length 526;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%; Score 73; DB 4; Length 717; 21.3%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 746;
63;
                                                                                                                                                                         Length 553
                                                                                                                                                                                                                                                                                                             Length 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.1%; Score 73; DB 4; Length 748; 23.3%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 73; DB 2; Length 750;
Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 788;
68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU36734 standard; protein; 792 AA.
Staphylococcus aureus cellular proliferation protein #904.
WO200170955-A2.
                                                                                                                                                                                                                             AAG24011 standard; protein; 556 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 27526.
EP1033405-A2.
                                                                   ABUJ1136 standard; protein; 553 AA.
Protein encoded by Prokaryotic essential gene #16663
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU42392 standard; protein; 788 AA.
Protein encoded by Prokaryotic essential gene #27919.
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                ABB71311 standard; protein; 717 AA.
Drosophila melanogaster polypeptide SEQ ID NO 40725.
WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 750 AA.
tissue secreted protein s195_10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73; DB 6;
Pred. No. 68;
                                                                                                                                                                         ; DB 6;
: 41;
                                                                                                                                                                                                                                                                                                             Score 73; DB 3;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-UL-1997.

(SMIK ) SMITHKLINE BEECHAM PLC.

Query Match
Similarity 23.3%; Pred. No.
                                                                                                                                                                         Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-711-1997.
(SMIK ) SMITHKLINE BEECHAM PLC.
(SMIK ) SMITHKLINE BEECHAM PLC.
ery Match 6.1%; Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW26672 standard; protein; 788 AA.
Staphylococcus aureus spoiliE protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus spoiliE protein. WO9726338-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW26673 standard; protein; 746 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEMY ) GENETICS INST INC. (GEMY ) GENETICS INST INC. (GEY MAtch ...) Arily 19.5%;
               Best Local Similarity 23.3%;
RESULT 879
                                                                                                                     PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 19.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001.
(ELIT-) ELITRA PHARM INC.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 886
                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW88407 standard;
Human adult neural
WO9857976-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9726338-A1.
                                                                                                                                                                                                                                                                                         06-SEP-2000.
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Best Loc RESULT 882

BBBBB

BBBBB

Length 966;

., 2

Length 966;

Length 845;

DB 4; Length 389;

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6.1%; Score 72.5; I
24.5%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-1994.
(TAKE ) TAKEDA CHEM IND LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-OCT-1994.
(TAKE ) TAKEDA CHEM IND LID.
Luery Match
Best Local Similarity
RESULT 906
ID ABP81865 stand>
DE Human oxytr
PD 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 911
                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
RESULT 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAY-2004.
(PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 914
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 909
                                                                                                                                                                                                                                                                                                   (PFIZ ) PFIZER LTD.
(PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                        07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72.5; DB 2; Length 389;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 325;
                                                                                                                                                                         Length 209;
                                                                                                                                                                                                                                                                                                       6.1%; Score 72.5; DB 6; Length 222; 20.5%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7; Length 353;
                                                                                                                                                                                                                ABU15302 standard; protein; 222 AA.
Protein encoded by Prokaryotic essential gene #829.
W0200277183-A2.
                                                                                                       M. tuberculosis and M. leprae marker protein #107.
WO200274903-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INEG) INRA INST NAT RECH AGRONOMIQUE.

ry Match

t Local Similarity 25.9%; Pred. No. 23;
                                                                                                                                                                             .,
                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 72.5; I
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                     PD 12-OCT-2001.
PA (IRRG) INRA INST NAT RECH AGRONOMIQUE.
Querry Match
Best Local Similarity 22.9%; Fred. No. 21;
RESULT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.1%; Score 72.5; I
25.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 72.5;
Pred. No. 25;
                                                                                                                                                                         Query Match 6.1%; Score 72.5;
Best Local Similarity 22.1%; Pred. No. 12;
RESULT 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH87557 standard; protein; 359 AA.
Enterococcus faecalis polypeptide #2037.
US6617156-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH87677 standard; protein; 353 AA.
Enterococcus faecalis polypeptide #2157.
US6617156-B1.
                                                    Best Local Similarity 19.5%; Pred. No. RESULT 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM40217 standard; protein; 389 AA.
Human polypeptide SEQ ID NO 3362.
WO200153312-A1.
CHVSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                      ABB53879 standard; protein; 307 AA.
Lactococcus lactis protein yfgG.
FR2807446-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR37264 standard; protein; 389 AA.
Oxytocin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB53675 standard; protein; 325 AA.
Lactococcus lactis protein ydhB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23832 standard; protein; 389 AA
                                                                                           ABU05456 standard; protein; 209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1%;
21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ROHT ) ROHTO PHARM CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-2003.
(DOUC/) DOUCETTE-STAMM L A.
(BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-2003.
(DOUC/) DOUCETTE-STAMM L A.
(BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ROHT ) ROHTO PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human oxytocin receptor. EP811684-A2.
                                                                                                                                                                                                                                                                             03-OCT-2002.
(ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L. F.

L.1997.

Lery Match

Lery Match

Best Local Similarity 2.

RESULT 905

ID AAM40217 stand**

PD E Human polyr*

PD 26-*

PA 26-*

PA
                                                                                                                                            26-SEP-2002.
(INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
RESULT 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FR2807446-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                          Query Match
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RESULT 901

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CS-OCT-1994.

(TAKE) TAKEDA CHEM IND LTD.

ery Match

for 18; Score 72.5; DB 2; Length 485;

ery Match

similarity 29.6%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.1%; Score 72.5; DB 8; Length 389; 24.5%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 8; Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 448;
                                                                                                                                                                                                                                                                                                                       DB 6; Length 389;
                                                                                                               Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 389
                                                                                                                                                                                                                                                                                                                                                                                                        Human oxytocin receptor (OXTR) protein SEQ ID NO:2. W02003993816-A2. 13-NOV-2003. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                  08-AUG-2002.
(LIFE-) LIFESPAN BIOSCIENCES INC.
(LIFE-) LIFESPAN BIOSCIENCES INC.
6.1%; Score 72.5; DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 72.5; DB 8; 24.5%; Pred. No. 29;
ABP81865 standard; protein; 389 AA.
Human oxytocin receptor protein SEQ ID NO:215.
WO200261087-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AARS8663 standard; protein; 476 AA.
Bovine PACAP receptor type 1A mature protein.
EP618291-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR58665 standard; protein; 448 AA.
Bovine PACAP receptor type 1B mature protein.
EP618291-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WOAVELLOOS.

(UYQU-) UNIV QUEBEC A MONTREAL.

(UYMO-) UNIV MONTREAL CENT HOSPITALIER.

(UYMO-) UNIV MONTREAL CENT HOSPITALIER.

6.1%; Score 72.5; DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     west match 6.1%; Score 72.5; Best Local Similarity 29.6%; Fred. No. 39; RESULT 913
                                                                                                                                                                                                                                                                                                                     6.1%; Score 72.5; 1
24.5%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.1%; Score 72.5;
Best Local Similarity 29.6%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR58657 standard; protein; 485 AA.
Bovine PACAP receptor type 1B protein.
EP618291-A2.
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Bovine PACAP receptor type 1A protein.
EP618291-A2
05-OCT-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD103915 standard; protein; 389 AA. Human oxytocin receptor polypeptide WO2004000993-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO29590 standard; protein; 389 AA.
Human GPCR OXTR, SEQ ID NO:692.
WO2004040000-A2.
                                                                                                                                                                                  AAE38317 standard; protein; 389 AA. Human oxytocin receptor protein. WO2003064402-A1.
                                                                                                                                                                                                                                                                                                                                                                                              ADF12125 standard; protein; 389 AA.
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ABJ18913 standard; protein; 453 AA.
Pathogen specific antigen related staphylococcal protein SEQ ID No 59.
WO200259148-A2.
30-MAR-2000.
(MILL-) MILLENNIUM PHARM INC.
lery Match 6.0%; Score 72; DB 3; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-0CT-2002.
A (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 453;
                                                                                                                                                                                                Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB 4; Length 414; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72; DB 3; Length 430;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 72; DB 6; Length 447; 23.9%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                   Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 72; DB 4; Length 448; 25.1%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 22.0%; Pred. No. 38;
RESULT 928
ID AAG50202 standard; protein; 430 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63591.
PN EP1013405-A2.
PD 06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG50203 standard; protein; 427 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 63592.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB62902 standard; protein; 448 AA.
Drosophila melanogaster polypeptide SEQ ID NO 15498.
WOZOOT11042-AZ.
27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU16441 standard; protein; 453 AA.
Protein encoded by Prokaryotic essential gene #1968.
WO200277183-A2.
                                                                                                                                                                                                                                                          protein; 396 AA.
Prokaryotic essential gene #5459
                                                                                                   AAW20731 standard; protein; 375 AA.
H. pylori inner membrane protein, 06cp11118orf6.
W09640893-A1.
                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 72; DB 3;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                   Score 72; DB 6;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                          DB '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB /
41;
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01-AUG-2002.

(CIST-) CISTEM BIOTECHNOLOGIES GMBH.

6.0%; Score 72;

lery Match amilarity 23.9%; Pred. No.
                                                                                                                                                                                                  Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                           ABG25051 standard; protein; 414 AA.
Novel human diagnostic protein #25042.
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM72825 standard; protein; 447 AA. Staphylococcus aureus protein #2065 WO200294868-A2.
                                                                                                                                                                                                                                                                                                      MOSCOLL
(BLIT-) BLITRA PHARM INC.
(BLIT-) BLITRA PHARM INC.
(BLIT-) BLITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%;
                                                                                                                                                                                                6.0%;
                                             Query Match
Best Local Similarity
RESULT 924
                                                                                                                                                                                                                                                      ABU19932 standard;
Protein encoded by
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY.
                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 925
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                            19-DEC-1996.
(ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       AAE31528 standard; protein; 848 AA.
Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.
WO200281696-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 MAY-1993.
(SANW ) SANWA KAGAKU KENKYUSHO CO.
ery Match 6.1%; Score 72.5; DB 2; Length 3010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 851;
                         6.1%; Score 72.5; DB 2; Length 513; 29.6%; Pred. No. 43;
                                                                                                                                                                                                                  Length 769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              848;
                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 848,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 72; DB 3; Length 334; 28.8%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 317;
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB53392 standard; protein; 334 AA.
Human colon cancer antigen protein sequence SEQ ID NO:932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU25159 standard; protein; 851 AA.
Protein encoded by Prokaryotic essential gene #10686.
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU39432 standard; protein; 317 AA.
Protein encoded by Prokaryotic essential gene #24959
WO200277183-A2.
                                                                                                                                                                                                                    DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR34580 standard; protein; 3010 AA.
Human hepatitis C virus gene encoded polypeptide
EP541089-A2.
                                                                                                                                                                                                                                                                        ABBO5429 standard; protein; 848 AA.
Arabidopsis thaliana ABH1 protein SEQ ID NO:2.
WO200196585-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2002.

(SYGN ) SYNGENTA PARTICIPATIONS AG.

ery Match

f.1%; Score 72.5; [

cry Match 22.3%; Pred. No. 86;
                                                                               ADIB1620 standard; protein; 769 AA.
C. elegans protein similar to Pfam PF00023.
US2004009537-A1.
                                                                                                                                                                                                                Query Match 6.1%; Score 72.5; 1
                                                                                                                                                                                                                                                                                                                                                                         6.1%; Score 72.5; I
22.3%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1%; Score 72.5; I 20.5%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72; DB
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY87505 standard; protein; 370 AA.
Human G coupled-protein receptor, hGR3.
WO200017641-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 72;
23.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB48543 standard; protein; 306 AA.
Listeria monocytogenes protein #1247.
WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
     (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002.
A (ELIT-) ELITRA PHARM INC.
Query Match 6.1
Best Local Similarity 20.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA
                                                                                                                                         15-JAN-2004.
(ROOS/) ROOS J.
(STAU/) STAUDERMAN K.
(VELI/) VELICELEBI G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2001.
(INSP ) INST PASTEUR.
Query Match
                                       Best Local Similarity RESULT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200055351-A1.
21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                 20-DEC-2001
                           Query Match
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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RESULT 919

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AAM93791 standard; protein; 208 AA.
Human polypeptide, SEQ ID NO: 3817.
           08-AUG-2002.
(LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WOZUCCO
17-FEB-2000.
(AGOU-) AGOURON PHARM INC.
ABTCh 6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%;
                                                                                                                                                          Best Local Similarity 20.8%;
RESULT 944
                                                                                                                                                                                                                                                                                                                                                                                                           (DECO-) DECODE GENETICS EHF
                                                                                     protein;
                                                                                                                                                  (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2001.
(PEKE) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BESULT 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 949
                                                                                     ADB67652 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human hARRG
                                                                                                                                   04-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
            ADN73057 standard; protein; 468 AA.
Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 952.
WO2004035798-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ69383 standard; protein; 594 AA.
Human heat mitochondrial protein as a therapeutic target SeqID1189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP97202 standard; protein; 696 AA.
Tumour-associated antigenic target protein TAT247 SEQ ID NO:84.
WO2003024392-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP97201 standard; protein; 696 AA.
Tumour-associated antigenic target protein TAT225 SEQ ID NO:83.
WO2003024392-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 696;
75;
                                                                                                  Score 72; DB 8; Length 468;
Pred. No. 43;
                                                                                                                                                                                                                                                                                                                     DB 3; Length 497;
47;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 6; Length 552;
. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 594
                                                                                                                                                                                                                Length 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGS0201 standard; protein; 556 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 63590.
EP1033405-A2.
                                                                                                                                                                                                                                                   AdG16337 standard; protein; 497 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 16944.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                          AAGI6336 standard; protein; 507 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 16943.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                  AAG16338 standard, protein; 495 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 16945.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 552 AA.
Prokaryotic essential gene #11265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7;
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
75;
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                            Score 72; DB 3;
Pred, No. 47;
23.9%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                    Score 72;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 72;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 72; 22.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP81969 standard; protein; 696 AA.
Human GPCR XPR1 protein SEQ ID NO:424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO20Usvc.
23-0CT-2003.
(MITO-) MITOKOR.
(BUCK-) BUCK INST AGE RES.
(ACK-) BUCK INST AGE RES.
                                                                                                                                                                                                                                                                                                                       6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%;
                                                                                                                                                                                                                 6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.0%;
Best Local Similarity 20.8%;
                                                                                                       Query Match
Best Local Similarity 21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002.
(ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2003.
(GETH ) GENENTECH INC.
                                                                          29-APR-2004.
(CROP-) CROPDESIGN NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 942
                                                                                                                                                                                                                        Best Local Similarity RESULT 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Best Local Similarity
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 936
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU25738 standard;
Protein encoded by
WO200277183-A2.
                                                                                                                                                                                                    06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2003
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                                                                                                                                                                                                                   Query Match
                 RESULT
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Score 72; DB 3; Length 2307;
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2307;
                                                                                     Human xenotropic& polytropic retrovirus receptor, SEQ ID 21
WO2003072824-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 72; DB 4; Length 1275; 19.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2307;
                                                                                                                                                                                                                                                                                                                                                                                                             AAB46702 standard; protein; 741 AA.
P. falciparum DNA polymerase protein fragment SEQ ID NO 11.
WO200075335-A2.
                                                                                                                                                                                                                                                                                                                              Cuery Match 6.0%; Score 72; DB 6; Length 724; Best Local Similarity 21.3%; Pred. No. 79; RESULT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 72; DB 4; Length 741; 30.4%; Pred. No. 81;
        DB 6; Length 696;
75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 788;
                                                                                                                                                       Length 696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABBS8917 standard; protein; 1275 AA.
Drosophila melanogaster polypeptide SEQ ID NO 3543.
WO200171042-A2.
                                                                                                                                                                                                                              ABM69179 standard; protein; 724 AA.
Photorhabdus luminescens protein sequence #2276.
WO200294867-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uuery Match 6.0%; Score 72; DB 3; Best Local Similarity 23.6%; Pred. No. 3.9e+02; RESULT 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72; DB 3;
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2001.
(BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
ery Match
ery Match
- roal Similarity 26.3%; Pred. No. 89;
                                                                                                                                                                      7;
                                                                                                                                                              DB 75;
                                                                                                                                                                    Score 72;
Pred. No.
Best Local Similarity 20.8%; Pred. No. RESULT 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70066 standard; protein; 2307 AA.
Recombinant fusion pHCAP-4 polyprotein.
WO200008469-A1.
(AGOU-) AGOURON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY70064 standard; protein; 2307 AA.
Recombinant fusion pHCAP-1 polyprotein.
W0200008469-A1.
(AGOU-) AGOURON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant fusion pHCAP-3 polyprotein, 7,000,008469-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM47977 standard; protein; 788 AA
                                                                      696 AA
                                                                                                                                                                                                                                                                                        28-NOV-2002.
(INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
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ADN38684 standard; protein; 382 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:2.
WO2003042661-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.0%; Score 71.5; DB 7; Length 382;
Best Local Similarity 22.3%; Pred. No. 37;
vuery Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 37;
RESULT 961.
                                                                                                                                                                              DB 6; Length 382;
                                                                                                                                                                                                                                                                                                                                          DB 6; Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 382,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7; Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 382,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABPB1876 standard; protein; 382 AA.
Human sphingolipid receptor Edg1 protein SEQ ID NO:237
WO200261087-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABRE5701 standard; protein; 382 AA.
Human endothelial differentiation sphingolipid GPCR
WO2003029277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                     PD 28-NOV-2002.

PA (AVET ) AVENTIS PHARM INC.

Query Match

6.0%; Score 71.5; E
BBST Local Similarity 22.3%; Pred. No. 37;

RESULT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD 10-APR-2003.
PA (RIGE-) RIGEL PHARM INC.
Querry Match
Best Local Similarity 22.3%; Pred. No. 37; RESULT 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%; Score 71.5; I 22.3%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 71.5; I
22.3%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.0%; Score 71.5; I 22.3%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                          6.0%; Score 71.5; 1
22.3%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71.5; 1
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 382 AA.
transcript seg id 72.
                                                                        ABP58069 standard; protein; 382 AA.
Human G-protein coupled receptor GAVE1
WO200295056-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB67662 standard, protein; 382 AA.

Human EDG1, SEQ ID 31.

N W02003072824-A1.

0 4-SEP-2003.

1 (SANY ) SANKYO CO LTD.

Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC40477 standard; protein; 382 AA.
Protein of human EDG-1.
WO2003052096-A1.
                                                                                                                                                                                                                                                                                                                                                                                                  protein; 382 AA.
                                                                                                                                                                                                                                        ABP59277 standard; protein; 382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-AUG-2002,
(LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-2003.
(TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PD 24-0CT-2002.

PA (RIGE-) RIGEL PHARM INC.
QUEYY MATCh 6.0%;

Best Local Similarity 22.3%;

RESULT 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                  ABU08809 standard; p:
Human EDG-1 protein.
US2002155512-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ45541 standard; p:
LXR-ligand induced t:
US2004023276-A1.
05-FEB-2004.
(WARD/) WARD T R.
                                                                                                                                                                                                                                                             Human Edg1 receptor. WO2003006503-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 968
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 963
                                                                                                                                                                                                                                                                                                  23-JAN-2003.
(CERE-) CERETEK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW37976 standard; protein; 342 AA.
Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.
WO9815289-A1.
                                                                                                     ADL31784 standard; protein; 208 AA.
Human protein encoded by a full length cDNA clone SeqID 3817.
Ep1396543-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 301;
                                                            DB 4; Length 208;
                                                                                                                                                                                                                                                                                                                                                           Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1998.
(CORR) CORNELL RES FOUND INC.
ETY Match
et Local Similarity 22.2%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 366;
                                                                                                                                                                                                                      Length 208,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG16922 standard; protein; 218 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 17750.
EP1033405-A2.
                                                                                                                                                                                                                                                                            AAGS6417 standard; protein; 209 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 72517.
BP103405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                     AAGS6416 standard; protein; 216 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 72516.
BP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU03456 standard; protein; 382 AA.
Angiogenesis-associated human protein sequence #1.
WO200279492-A2.
10-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 71.5; DB 2; 23.1%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-CCT-2001.
(INRG ) INRA INST NAT RECH AGRONOMIQUE.
ery Match
6.0%; Score 71.5; E
                                                          Query Match 6.0%; Score 71.5; 1
Best Local Similarity 25.2%; Pred. No. 16;
                                                                                                                                                                                                                 6.0%; Score 71.5; 1
25.2%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 71.5; I
25.6%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.0%; Score 71.5; I 25.6%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 71.5; 1
42.4%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.0%; Score 71.5; 1
Best Local Similarity 21.0%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR88410 standard; protein; 366 AA.
High-affinity melatonin-la receptor.
WO9535320-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-1995.
(MASS-) MASSACHUSETTS GEN HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB53486 standard; protein; 301 AA.
Lactococcus lactis protein ybiG.
FR2807446-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG87423 standard; protein; 348 AA.
Meloidogyne incognita plk1 protein.
US2003150017-A1.
                                                                                                                                                                                10-MAR-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                  05-SEP-2001.
(HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2003.
(MESA/) MESA J R B.
(GRAH/) GRAHAM M W.
(FAIR/) FAIRBAIRN D J.
                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 953
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
  EP1130094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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RESULT 958

RESULT 959

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03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
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6.0%; Score 71.5; DB 6; Length 565;
ry Match
t Local Similarity 22.4%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 524;
                                                                                                                                                                                                                                                                                                                                  DB 7; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 441;
                                                                                                                                                                                            6.0%; Score 71.5; DB 5; Length 390; 22.2%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 435;
                                                         Length 382;
                                                                                                                          Catostomus commersoni isotocin receptor protein SEQ ID NO:3. WO200192296-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABJ37074 standard; protein; 565 AA.

Human breast cancer / ovarian cancer related protein #50.
WO2003000012-A2.
03-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABUZ6033 standard; protein; 524 AA.
Protein encoded by Prokaryotic essential gene #11560.
W0200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABŪ16392 standard; protein; 603 AA.
Protein encoded by Prokaryotic essential gene #1919.
W0200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARR22000 standard; protein; 441 AA.
Partial M17 antigen from Region II, encoded by PCR
W09203457-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP75877 standard; protein; 470 AA.
Human secretory polypeptide SPTM SEQ ID NO 1061.
WO200283876-A2.
                                                              DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-1998.
4 (HUMA-) HUMAN GENOME SCI INC.
6.0%; Score 71.5; I Guery Match
9est Local Similarity 22.4%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 22.4%; Pred. No. 50;
RESULT 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2002.
(BLIT-) BLITRA PHARM INC.
(ELIT-) BLITRA PHARM INC.
(OR; Score 71.5; I
(ery Match 26.6%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.0%; Score 71.5; Best Local Similarity 22.6%; Pred. No. 45; RESULT 974
                                                                                                                                                                                                                                                                                                                                      6.0%; Score 71.5; 1
22.7%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 71.5; 21.4%; Pred. No. 45;
                                                           Score 71.5; 1
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW51244 standard; protein; 568 AA. Human calcitonin receptor. W09821242-A1.
                                                                                                                                                                                                                                                  ADM83141 standard; protein; 394 AA. Rat vesicle membrane protein (VMP)2. US2003175787-A1.
                                                                                                                                                                                                                                                                                                                                                                                   ABB48023 standard; protein; 435 AA.
Listeria monocytogenes protein #727
WO200177335-A2.
                                                                                                                 ABB05226 standard; protein; 390 AA.
                                                                6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1992.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                (INSP) INST PASTEUR. Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 977
                                                                                                                                                                                                                                                                                                           18-SEP-2003.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                (MAOM/) MAO M.
(LINS/) LINSLEY P S.
(LUND/) LUND E.
                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 971
                                                                                Best Local Similarity
                                                                                                                                                                      06-DEC-2001.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                    Query Match
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DB 7; Length 698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 697;
                                                                                                                                                                                                                                                                                                              DB 7; Length 697;
                                                                                                                            Length 603;
   Length 603;
                                                                                                                                                                                                                                                                                                                                                       ADM43217 standard; protein; 697 AA.
Human methionine synthase reductase del Leu 576 variant.
US2003082676-A1.
01-MAY-2003.
                                                                                                                                                                     ADM43215 standard; protein; 697 AA.
Human methionine synthase reductase del Arg 559 variant.
US2003082676-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM43213 standard; protein; 698 AA.
Human methionine synthase reductase Cys37Tyr variant.
US2003082676-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADVINASZII Standard; protein; 698 AA.
Human methionine synthase reductase Met22Ile variant.
US2003082676-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB07591 standard; protein; 698 AA.
A human methionine synthase reductase polypeptide.
WO200042196-A2.
Score 71.5; DB 6;
Pred. No. 70;
                                                                                                                              9
                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 71.5; 1
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.0%; Score 71.5; 1
22.8%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 71.5; 1
22.8%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71.5; 1
Pred. No. 86;
                                                                                                                            Score 71.5;
Pred. No. 70;
                                                                                                                                                                                                                                                                                                                6.0%; Score 71.5;
22.8%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein; 698 AA.
Novel human diagnostic protein #874.
W0200175067-A2.
11-OCT-2001.
(HYSE) HYSEQ INC.
                                                 ABM72619 standard; protein; 603 AA. Staphylococcus aureus protein #1859. WO200294868-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%;
                                                                                                                               6.0%;
      6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GRAV) GRAVEL R A.
(ROZE) ROZEN R.
(LECL) LECLERC D.
(HILS!) WILSON M.
(ROSE) ROSENBLATT D.
                                                                                                                                                                                                                                                                                                                                                                                                                       (GRAV) GRAVEL R A.
(ROZE) ROZEN R.
(LECL) LECLERC D.
(WILS) WILSON A.
(ROSE)) ROSENBLAIT D.
                                                                                                                                                                                                                         01-MAY-2003.
(GRAV) GRAVEL R A.
(ROZE) ROZEN R.
(LECL) IECLERC D.
(WILS) WILSON A.
(ROSE)) ROSENBLATT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-2000.
(UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 983
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                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 982
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RESULT 984
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(LECL/) LECLERC D.
(WILS/) WILSON A.
                                                                                                                                            Local Similarity
                Best Local Similarity RESULT 979
                                                                                                                CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2003
                                                                                                   28-NOV-2002
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                                                                                                                                  Query Match
         Query Match
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RESULT 985
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ADL22689 standard; protein; 2245 AA.
Human disease detection and treatment (MDDT) protein - SEQ ID 138.
WO2003062379-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.-UL-2003.

(INCY-) INCYTE GENOMICS INC.

6.0%; Score 71.5; DB 7; Length 2245;

lery Match 22.4%; Pred. No. 4.38+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 71.5; DB 3; Length 2405;
Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 71.5; DB 4; Length 2560; Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                             GO-MAR-2000.
(UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
ery Match 6.0%; Score 71.5; DB 3; Length 890;
               Query Match 6.0%; Score 71.5; DB 7; Length 698; Best Local Similarity 22.8%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 71.5; DB 7; Length 890;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                          DB 7; Length 698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB42192 standard; protein; 2405 AA.
Human ORFX ORF1956 polypeptide sequence SEQ ID NO:3912.
WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB78282 standard; protein; 890 AA.
Amino acid sequence of human wolframin polypeptide.
WO200263307-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 71.5; DB 7;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 71.5; DB 5;
23.8%; Pred. No. 1.2e+02;
                                                     Human wild-type methionine synthase reductase. US200382676-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB11404 standard; peptide; 2560 AA.
Human FLAMINGO 1 homologue, SEQ ID NO:1774.
WO200157188-A2.
                                                                                                                                                                                                                                        6.0%; Score 71.5; 1
22.8%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MP53 protein sequence SEQ ID NO:97. W020030883047-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD46013 standard; protein; 890 AA.
Human Protein 076024, SEQ ID NO 11685.
WO2003016475-A2.
                                                                                                                                                                                                                                                                                            AAYS1606 standard; protein; 890 AA.
Human wml protein.
D819845277-C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-2002.
(PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.0%;
Best Local Similarity 22.4%;
RESULT 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.0%;
Best Local Similarity 23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.0%;
Best Local Similarity 22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                          (GRAV) GRAVEL R A.
(ROZE) ROZEN R.
(LECL) LECLERC D.
(WILS) WILSON A.
(ROSE/) ROSENBLATT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-OCT-2000.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-2003.
(EXEL-) EXELIXIS INC.
(ROSE/) ROSENBLATT D.
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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RESULT 990
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AAM50866 standard; protein; 2923 AA.
Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.
WO200208765-A2.
                               PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 6; Length 2894;
Best Local Similarity 22.4%; Pred. No. 6.2e+02;
RESULT 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 71.5; DB 7; Length 2923;
Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                 Length 2923;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2923;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2923;
                                                                                                                                                            AAU07054 standard; protein; 2923 AA.
Human Flamingo protein encoded by cDNA splice variant
WO200161003-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC15499 standard; protein; 2923 AA.
Human cadherin EGF LAG seven-pass G-type receptor
US2003086934-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
QUETY MAtch
6.0%; Score 71.5; DB 7; L
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
RESULT 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PA (RING)) RING B.
PA (ROSS/) ROSS D.
PA (SEIT/) SETTZ R.
PA (VRIJ/) VAN DE RIJN J M.
Query March
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
RESULT 999
ID ADC86479 standard; protein; 2923 AA.
PB Human GPCR protein SEQ ID NO:932.
PR EP1270724-A2.
                                                                                                                                                                                                                PA (STRD ) UNIV STANFORD.
PA (GENO-) APPLIED GENOMICS INC.
Query Match
Best Local Similarity 22.4%; Pred. No. 6.38+02;
RESULT 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.0%; Score 71.5; DB 6; Best Local Similarity 22.4%; Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71.5; DB 7;
Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP82018 standard; protein; 2923 AA.
Human GPCR CELSR2 protein SEQ ID NO:524.
WO200261087-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE5407 standard; protein; 2923 AA.
Human Protein XP_042739, SEQ ID NO 210.
WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE5411 standard; protein; 2923 AA.
Human Protein XP_042739, SEQ ID NO 214.
WO2003016475-A2.
ABU11556 standard; protein; 2894 AA.
Human MDDT polypeptide SEQ ID 503.
WO200279449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-2002.
(LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                Best Local Similarity
RESULT 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BOTS/) 1
(BROW/) 1
(PERO/) 1
(RING/) 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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17-MAR-1994
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                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 71.5; DB 4; Length 5303; 29.5%; Pred. No. 1.40+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3011;
                                                                                                                  6.0%; Score 71.5; DB 8; Length 2923; 22.4%; Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2956;
                                                                                                                                                                                                                                                                             Length 2936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-2001.
(BODE-) BODE GENE DEV CO LTD SHANGHAI.
ery Match 5.9%; Score 71; DB 5; Length 198;
or Lonal Similarity 24.5%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.9%; Score 71; DB 6; Length 240; Best Local Similarity 18.6%; Pred. No. 22; RESULT 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71; DB 5; Length 295;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARR34468 standard; protein; 3011 AA.
Encoded by full-length Hepatitis C virus clone JK1-B.
JP05068562-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB67866 standard; protein; 5303 AA.
Drosophila melanogaster polypeptide SEQ ID NO 30390
WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                          PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 22.4%; Pred. No. 6.4e+02;
RESULT 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%; Score 71.5; DB 2; 22.8%; Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                             Query Match 6.0%; Score 71.5; DB 5;
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABBO6793 standard; protein; 198 AA.
Human transmembrane 4 protein 22 SEQ ID NO:2.
CN1327990-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP26255 standard; protein; 295 AA.
Streptococcus polypeptide SEQ ID NO 1686.
WQ200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU07053 standard; protein; 2956 AA.
Human Flamingo polypeptide.
WO200161003-A1.
                  AD029245 standard; protein; 2923 AA.
Human GPCR CELSR2, SEQ ID NO:346.
W02004040000-A2.
                                                                                                                                                                           AAU74826 standard; protein; 2936 AA.
Human REPTR 9 protein.
WO200198354-A2.
27-DEC-2001.
(INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR58398 standard; protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 23-MAR-1993.

PA (SANW ) SANWA KAGAKU KENKYUSHO CO.

Query Match 6.0%; Score

Best Local Similarity 23.7%; Pred.

RESULT 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO20uc2.
02-MAY 2002.
(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
(GENO-) INST GENOMIC RES.
5.9%; SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 2
RESULT 1009
ID ABR58398 standard; pro
DE Human NOV17a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JAN-1993.
(CHIR ) CHIRON CORP.
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
                                                                                   13-MAY-2004.
(PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
RESULT 1002
1D ADO2924!
DE Human GI
PN WO200404
PD 13-MAY-2
PA (PRIM-)
                                                                                                                                                                  RESULT 1003
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AAG72952 standard; protein; 310 AA.
Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.
WO200127158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.9%; Score 71; DB 5; Length 423; Best Local Similarity 28.4%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.9%; Score 71; DB 4; Length 312; 22.9%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                   Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Query Match

Query Match

Query Match

Query Match

Dest Local Similarity 19.7%; Pred. No. 32;

RESULT 1014

ID AAG72169 standard; protein; 312 AA.

DE Human olfactory receptor polypeptide, SEQ ID NO: 1850.

PD 19-APR-2001.

PA (DIG!-) DIGISCENTS.

PA (DIG!-) DIGISCENTS.

PA (TEDA) YEDA RES & DEV CO LTD.

Query Match

Query Match

Best Local Similarity 22.9%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1015
ID AAG72217 standard; protein; 312 AA.
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2058
PN WO200127158-A2.
                                                                                                                                      Length 310;
                                                                      PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (VEDA) YEDA RES & DEV CO LTD.
Query Match
Best Local Similarity 22.9%; Score 71; DB 4; Length 3
RESULT 1012
ID ARA4817 standard; protein; 312 AA.
DE G-protain coupled human interleukin-8 receptor protein.
PN W09405695-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us6673910-B1.

PD 06-JAN-2004.

PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match
Best Local Similarity 38.0%; Pred. No. 49;
RESULT 10.9

ID ADJ55142 standard; protein; 444 AP

PD Novel NOVX protein sequence

PD 15-MAY-200^2

PA (FENDAL 200^2)

PA 15-MAY-200^2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 20.3%; Pred. No. 44;
RESULT 1017
                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                       AANOZ689 standard; peptide; 312 AA.
G-protein coupled human interleukin-8 receptor.
US5508384-A.
                                                                                                                                                                                                                                                                                             (UNIV) UNIV NEW YORK STATE.

17 Match

15.9%; Score 71;

14 Local Similarity 19.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB48413 standard; protein; 423 AA.
Listeria monocytogenes protein #1117.
W0200177335-A2.
18-OCT-2001.
(INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB54394 standard; protein; 391 AA.
Lactococcus lactis protein ykiI.
FR2807446-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (VEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1016
                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
RESULT 1013
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AAY90640 standard; protein; 471 AA.
Human G protein-coupled receptor 5HT-2A (serotonin receptor)
WO200022129-A1.
                                                                                                                                         Query Match
Best Local Similarity 21.0%; Pred. No. 52;
RESULT 1021
ID ADP29417 standard; protein; 455 AA.
DE Human secreted protein SEQ ID #184.
PN WOO040435732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 24.3%; Pred. No. 54;
RESULT 1022
 Score 71; DB 7; Length 444;
Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.9%; Score 71; DB 2; Length 471; Best Local Similarity 23.7%; Pred. No. 57; RESULT 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wurry Match 5.9%; Score 71; DB 3; Length 471; Best Local Similarity 23.7%; Pred. No. 57; RESULT 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 6; Length 457;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71; DB 8; Length 470;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 471;
57;
                                                                                                                                                                                                                                                                                                                                            ABU19912 standard; protein; 457 AA.
Protein encoded by Prokaryotic essential gene #5439.
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human endogenous SHT2A serotonin receptor.
US2003224442-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9%; Score 71; DB 23.7%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 71;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW23781 standard; protein; 471 AA.
Human serotonin 5-HT2 receptor protein.
US5661024-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
Query Match 5.9%; Score 71;
                                                     ADJ95144 standard; protein; 444 AA. Novel NOVX protein sequence #186. WO20030404035-A2. IS-MAY-2003. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR37659 standard; protein; 471 AA.
Seguence encoded by cDNA.
WO9311257-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW77107 standard; protein; 471 AA.
Human 5-HT2A serotonin receptor.
WO9838217-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI24575 standard; protein; 470 AA.
     5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1997.
(SYNA-) SYNAPTIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%;
                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-SEP-1998.
(TEIT/) TEITLER M.
(HERR/) HERRICK-DAVIS K.
(EGAN/) EGAN C C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2000.
(AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BEHA) BEHAN D P.
(CHAL/) CHALMERS D T.
(LIAM) LIAM C W.
(RUSS/) RUSSO J F.
(THOM/) THOMSEN W J.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1023
Query Match
Best Local Similarity
RESULT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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ID AAY90675 standard; protein; 471 AA.

DE Human mutant G protein-coupled receptor 5HT-2A.

PN W0200022129-A1.

PD 20-APR-2000.

PA (AREN-) ARENA FHARM INC.

Query Match

5.9%; Score 71; DB 3; Length 471;

Best Local Similarity 23.7%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.9%; Score 71; DB 7; Length 471; BBst Local Similarity 23.7%; Pred. No. 57; RESULT 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 57;
RESULT 1035
                                                                                                                                                                                                                                                                                                            Score 71; DB 5; Length 471; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 29-APR-2003.

PA (AREN-) ARENA PHARM INC.

Query Match
5.9%; Score 71; DB 7; Length 471;

Best Local Similarity 23.7%; Pred. No. 57;

RESULT 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.94; Score 71; DB 7; Length 471; Best Local Similarity 23.74; Pred. No. 57; RESULT 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%; Score 71; DB 7; Length 471; 23.7%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC22641 standard; protein; 471 AA.
Human G protein-coupled receptor (GPCR) polypeptide #32.
US6555339-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC22747 standard; protein; 471 AA.
Human G protein-coupled receptor (GPCR) polypeptide #72
US6555339-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.9%; Score 71; DB
Best Local Similarity 23.7%; Pred. No. 57;
RESULT 1031
                                                                                                                                                                                                                                                                                                                                                                            ABPB1765 standard; protein; 471 AA.
Human 5-HT2A receptor protein SEQ ID NO:12.
WO200261087-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE65844 standard; protein; 471 AA. Human serotonin 2A receptor. US200317073-A1. (SAPP-2003. (SATO/) SATO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH14220 standard; protein; 471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL90125 standard; protein; 471 AA.
Human serotonin receptor 5HT2a.
US2003167476-A1.
                                                                                                                                                                                                  ABB07978 standard; protein; 471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADH14114 standard; protein; 471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutated human serotonin SHT_ZA.
US2003105292-A1.
                                                                                                                                                                                                                        Human 5-HT2 receptor sequence.
                                                                                                                                                                                                                                                                                                                 5.9%;
                                                                                                                                                                                                                                                                                       (SYNA-) SYNAPTIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-APR-2003.
(AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human serotonin 5HT_2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LIAW/) LIAW C W.
(BEHA/) BEHAN D P.
(CHAL/) CHALMERS D T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LIAW/) LIAW C W.
(BEHA/) BEHAN D P.
(CHAL/) CHALMERS D T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-2003.
(CONK/) CONKLIN B R.
                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003105292-A1.
                                                                                                                                                                                                                                             US6383762-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-AUG-2002
                                                                                                                                                                                                                                                                    07-MAY-200
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10-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 6; Length 559;
Pred. No. 72;
                                                                                                                                                                                                                                         23-MAR-1999.
(SYNA-) SYNAPTIC FHARM CORP.
ery Match 5.9%; Score 71; DB 2; Length 478;
ery Match 23.7%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR.

(CORGS) CNRS CENT NAT RECH SCI.

ry Match

t Local Similarity 23.5%; Pred. No. 61;
   DB 7; Length 471;
57;
                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 71; DB 5; Length 480; 23.7%; Pred. No. 58;
                                                                                                                                    Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 545; 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ26399 standard; protein; 559 AA.
Aspergillus fumigatus essential gene protein #1057
WO200286090-A2.
                                                                                                                                                                                       AAYO1626 standard; protein; 478 AA.
Amino acid sequence of the human 5-HT2 receptor.
US5885785-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM70440 standard; protein; 493 AA.
Photorhabdus luminescens protein sequence #3537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , DB 7;
                                                                                                                                         8
                                                                                                                                        DB
57;
                                                                                                                                        Score 71;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 71;
Pred. No.
     Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.9%; Score 71; 22.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD48660 standard; protein; 545 AA.
Rat Protein BAA25372, SEQ ID NO 14366.
WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP35686 standard; protein; 563 AA.
Fungal ZBC protein sequence #112.
WO200224865-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB20578 standard; protein; 564 AA. Mouse OCTN3 protein SEQ ID NO:1. WO200046368-A1.
                                                                                                                                                                                                                                                                                                                     ABG70577 standard; protein; 480 AA.
Human serotonin (5-HT2) receptor.
US2002098548-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADESG383 standard; protein; 545 AA.
Rat Protein 070536, SEQ ID NO 2235.
W02003016475-A2.
                                                   AD029506 standard; protein; 471 AA. Human GPCR HTRZA, SEQ ID NO:608. W02004040000-A2. 13-MAY-2004. (PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ry Match
ry Match
rocal Similarity 23.1%;
       5.9%;
                                                                                                                                         5.9%;
                                                                                                                                                                                                                                                                                                                                                                                   25-JUL-2002.
(SYNA-) SYNAPTIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D 27-FEB-2003.
A (GEHO ) GEN HOSPITAL CORP.
A (FARB ) BAYER AG. 5.9%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
   Query Match
Best Local Similarity 2
IDSULT 1037
ID AD029506 standard; pro
DE Human GPCR HTR2A, SEQ
PN W02004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2002.
(MICR-) MICROBIA INC.
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1039
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 1044
                                                                                                                                         Query Match
Best Local Similarity
RESULT 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200294867-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1042
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Length 3010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 71; DB 2; Length 3010;
Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 8; Length 727; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 792;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 727;
                                                                                                                                                                                                                                                                                     Length 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH76500 standard; protein; 727 AA.
727 amino acid human neurotransmitter transporter protein.
US2003219774-A1.
                 Length 564;
                                                                                                                                                    Length 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -A-310616 standard; protein; 3010 AA.
AAR30616 standard; protein; 3010 AA.
Polypeptide coded by Korean HCV full cDNA sequence LBC1
BP521318-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB60052 standard; protein; 792 AA.
Drosophila melanogaster polypeptide SEQ ID NO 6948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%; Score 71; DB 2; 1
26.9%; Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.9%; Score 71; DB 7; I
24.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.9%; Score 71; DB 4;
17.7%; Pred. No. 1.2e+02;
CHUGAI RES INST MOLECULAR MEDICINE INC.
5.9%; Score 71; DB 3; 1
Similarity 21.4%; Pred. No. 73;
                                                                                                                                                                                                                                                                                        DB 5;
1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 71; DB 6; 24.3%; Pred. No. 1e+02;
                                                                                                                                                    5.9%; Score 71; DB 5; 22.3%; Pred. No. 94;
                                                                   ABB91532 standard; protein; 676 AA.
Herbicidally active polypeptide SEQ ID NO 743.
W0200210210-A2.
(FBB-2002.
(FABB ) BAYER AG.
                                                                                                                                                                                                                                                                                        Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AARS5417 standard; protein; 3010 AA.
Blood transmiscible NANBHV protein.
JP06105690-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human neurotransmitter transporter. WO2003059947-A1.
                                                                                                                                                                                                                                                                                                                                      ABU54636 standard; protein; 727 AA.
Human NOVX polypeptide #95.
WO200281498-A2.
                                                                                                                                                                                     RESULT 1047
ID AAE21800 standard; protein; 727 AA.
DE Human HIPHUM 0000029 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.9%;
                                                                                                                                                                                                                                                GB2305---
20-FEB-2002.
(GLAX ) GLAXO GROUP LTD.
5 9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RAMA/) RAMANATHAN C S. (WEST/) WESTPHAL R. (FEDE/) FEDER J N. (LEEL/) LEE L M.
                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1048
                 Query Match
Best Local Similarity
RESULT 1046
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JAN-1993.
(LUCK-) LUCKY LTD.
                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-1994.
(KAEN/) KAENNO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) 24-JUL-2003.
A (FARB ) BAYER AG.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-2003.
(SHAR/) SHARMA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                         Query Match
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PPREE

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ADI35077 standard; protein; 365 AA.
Human prostaglandin E receptor subtype BP3 (PTGER3) protein #9
US2003224393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR69518 standard; protein; 365 AA.
Prostaglandin-EP3-9 receptor.
W09500552-A1.
W09500552-A1.
(NGN-1995.
(WERI ) MERCK FROSST CANADA INC.
Ery Match
S.9%; Score 70.5; DB 2; Length 365; st Local Similarity 24.2%; Pred. No. 46;
Query Match 5.9%; Score 70.5; DB 6; Length 297; Best Local Similarity 24.1%; Pred. No. 34; RESULT 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vuery Match 5.9%; Score 70.5; DB 8; Length 343;
Best Local Similarity 30.0%; Pred. No. 42;
RESULT 1067
                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 5.9%; Score 70.5; DB 8; Length 330; Best Local Similarity 24.2%; Pred. No. 40; RESULT 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.9%; Score 70.5; DB 8; Length 365; Best Local Similarity 24.2%; Pred. No. 46;
                                                                                                                                                                                                           Length 321
                                                                                                                                                                                                                                                                             ADH22355 standard; protein; 330 AA.
Human receptor & membrane associated protein (REMAP) SeqID5
WO2003104395-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8; Length 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH72226 standard; protein; 343 AA.
Human protein of the invention NOV55a SEQ ID NO:1122.
WO2003102155-A2.
                                                                                                                                                                                                             DB 6;
                                                               DE ABMO1358 standard; protein; 321 AA.

DE Photorhabdus luminescens protein sequence #3455.

PN W0200294867-A2.

PD 28-NOV-2002.

PA (INSP ) INST PASTEUR.

PA (CNRS ) CNRS CENT NAT RECH SCI.

Query Match 5.9%; Score 70.5; DB 6;

Best Local Similarity 19.2%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID ARBSEL standard; protein; 365 AA.

ID Human PTGER3 protein isoform, EP3b.

DE Human PTGER3 protein isoform, EP3b.

PN WO2003064471-A2.

PD 07-AUG-2003.

PA (DECO-) DECODE GENETICS EHF.

QUETY MATCh

Best Local Similarity 24.2%; Pred. No. 46; BESULT 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70.5; I
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL15889 standard; protein; 365 AA. Human prostaglandin EP3 receptor #3. US6670134-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK68232 standard; protein; 343 AA.
Novel NOVX protein #79.
WO2003085124-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF04358 standard; protein; 367 AA.
Bacterial polypeptide #471.
US6605709-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.9%;
Best Local Similarity 30.0%;
RESULT 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-DEC-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                             18-DEC-2003.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYAR-) UNIV ARIZONA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                     AAU97208 standard; protein; 228 AA.
Portion of a wheat sugar transport protein encoded by wreln.pk0006.b4.
US6383776-B1.
                                                                                                                                                                                   AAU01287 standard; protein; 218 AA.
Brassica napus fatty acid desaturase, Fad3C, partial sequence.
WO200125453-A2.
12-ARR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 26-DEC_2002.
PA (HELEV) HELENTJARIS T G.
Query Match 5.9%; Score 70.5; DB 8; Length 228;
Best Local Similarity 21.6%; Pred. No. 24;
RESULT 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 22.8%; Score 70.5; DB 6; Length 275;
RESULT 1060

ID ABB55033 standard; protein; 285 AA.

DE Lactococcus lactis protein malG.
PN FR2807446-A1.
PD 12-CCT-2001.
PD 12-CCT-2001.
PA GING ) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 26.1%; Pred. No. 32;
                                                                                                                                                                                                                                                                             (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match
Best Local Similarity 29.3%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 70.5; DB 5; Length 291; 29.4%; Pred. No. 33;
                                                                                                                      DB 6; Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB05467 standard; protein; 291 AA.
Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.
JP2001321171-A.
20-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABUI1430 standard; protein; 275 AA.
Protein encoded by Prokaryotic essential gene #2957.
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG47920 standard; protein; 228 AA.
Wheat Arabidopsis-like sugar transport protein #3
US2002199217-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                (07-MAX-2002.

(DUPO ) DU PONT DE NEMOURS & CO E I.

5.9%; Score 70.5; I

5.3%; Pred. No. 24;
                                                                                                          Query Match
Best Local Similarity 26.5%; Pred. No. 20;
RESULT 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70.5; I
Pred. No. 24;
  ABR83573 standard; protein; 202 AA.
BcrC amino acid sequence SEQ ID NO:40.
W0200357708-A2.
17-JUL-2003.
(UYNE-) UNIV NEWCASTLE VENTURES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA35787 standard; protein; 297 AA.
Acinetobacter baumannii protein #2948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wheat sugar transport protein #3.
US2002178468-A1.
28-NOV-2002.
(ALLE/) ALLEN S M.
(HITZ/) HITZ W D.
(KINN/) KINNEY A J.
(TING/) TINGEY S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU08333 standard; protein; 228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAY-2003. (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WARI/) WARIISHI H.
(KUBI ) KUBOTA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1056
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Best Local Similarity
RESULT 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6562958-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
RESULT 1062
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ADISO75 standard; protein; 374 AA.
Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8
US2003224393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.9%; Score 70.5; DB 8; Length 388; Best Local Similarity 24.2%; Pred. No. 50; RESULT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI35061 standard; protein; 388 AA.
Human prostaglandin E receptor subtype EP3 (PTGER3) protein
US2003224393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 70.5; DB 8; Length 388;
24.2%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 17-MAR-1994.
PA (UYNY) UNIV NEW YORK STATE.
Guery Match 5:9%; Score 70.5; DB 2; Length 379;
Best Local Similarity 22.9%; Pred. No. 48;
RESULT 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%; Score 70.5; DB 2; Length 388; 24.2%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7; Length 388;
(GENO-) GENOME THERAPEUTICS CORP.

ry Match 5.9%; Score 70.5; DB 7; Length 367; t Local Similarity 33.3%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 379;
                                                                                                                                                                                                                                                                                                                                                        DB 8; Length 374;
                                                                                                                                                                                      DB 7; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                   AAR48711 standard; protein; 379 AA.
G-protein coupled rat serotonin 2 receptor protein
WO9405695-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW02683 standard; peptide; 379 AA.
G-protein coupled rat serotonin 2 receptor.
US5508384-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match
Best Local Similarity 24.2%; Pred. No. 50; RESULT 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%; Score 70.5; I 22.9%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                        5.9%; Score 70.5; I
24.2%; Pred. No. 47;
                                                                                                                                                                                      5.9%; Score 70.5; 24.2%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL15887 standard; protein; 388 AA. Human prostaglandin EP3 receptor #2. US6670134-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR69516 standard; protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR65517 standard; protein; 388 AA.
Prostaglandin-EP3-21 receptor.
WO9500552-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE38513 standard; protein; 388 AA.
Human PTGER3 protein isoform, EP3c.
WO2003064471-A2.
                                                                                 AAE38520 standard; protein; 374 AA.
Human PTGER3 protein isoform, EP3d.
WO2003064471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostaglandin-EP3-alpha receptor. 05-JAN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MERI ) MERCK FROSST CANADA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2003.
(DECO-) DECODE GENETICS EHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-1996.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                     04-DEC-2003.
(DECO-) DECODE GENETICS EHF.
                                                                                                                                                   07-AUG-2003.
(DECO-) DECODE GENETICS EHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-2003.
(ALLR ) ALLERGAN INC.
(UYAR-) UNIV ARIZONA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1077
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                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1073
                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                               Query Match
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AUI35067 standard; protein; 390 AA.
Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.
US2002224393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI35069 standard; protein; 390 AA.
Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.
US2003224393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 24.2%; Score 70.5; DB 8; Length 390; RESULT 1085

ID ADLISOS standard; protein; 390 AA.

DE Human prostaglandin EP3 receptor #4.

PN US6670134-B1.

PD 30-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'7-AUG-2003.
(DECO-) DECODE GENETICS EHF.
6ry Match
-- Tonal Similarity 24.2%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.9%; Score 70.5; DB 8; Length 390; Best Local Similarity 24.2%; Pred. No. 50; RESULT 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.9%; Score 70.5; DB 8; Length 390; Best Local Similarity 24.2%; Pred. No. 50; RESULT 1087
                                                                                                                                                  PA (DECO-) DECODE GENETICS EHF.
Query Match
5.9%; Score 70.5; DB 7; Length 390;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Ouery Match
Best Local Similarity 24.2%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 390;
                    DB 2; Length 390;
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ID AAE38519 standard; protein; 393 AA.

DE Human PTGER3 protein isoform, EP3e.

PN WQ2003064471-A2.
(MERI ) MERCK FROSST CANADA INC.
ry Match
5.9%; Score 70.5; I
t Local Similarity 24.2%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 24.2%; Pred. No. 50; RESULT 1083
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Human PTGER3 protein isoform, EP3-VI.
WO2003064471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM57411 standard; protein; 393 AA.
Human prostaglandin EP3-VI receptor.
JP10113185-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL15885 standard; protein; 390 AA. Human prostaglandin EP3 receptor #1. US6670134-B1.
                                                                                                                                                                                                                                                            AAE38517 standard; protein; 390 AA.
Human PrGER3 protein isoform, EP3a2.
WO2003064471-A2.
                                                                                    AAE38516 standard; protein; 390 AA.
Human PTGER3 protein isoform, EP3a1
WO2003064471-A2.
                                                                                                                                                                                                                                                                                                                                 07-AUG-2003.
(DECO-) DECODE GENETICS EHF.
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(ONOY ) ONO PHARM CO LID.
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(ALLR ) ALLERGAN INC.
(UYAR-) UNIV ARIZONA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALLR ) ALLERGAN INC. (UYAR-) UNIV ARIZONA.
                                           Best Local Similarity RESULT 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                             Query Match
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(DECO-) DECODE GENETICS EHF.
                             Query Match
Best Local Similarity
RESULT 1099
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Best Local Similarity
RESULT 1105
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Best Local Similarity
RESULT 1102
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RESULT 1100
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                                                                                                                               ADI35063 standard;
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Protein #69 with increased gene expression in renal cell carcinoma.
WO2004032842-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI35079 standard; protein; 402 AA.
Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10
US2003224393-A1.
                                                                                                                                                                             Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11 US2003224393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7 US2003224393-A1.
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Pred. No. 52;
                                                                 DB 7; Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70.5; DB 8; Length 393;
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     '5.9%; Score 70.5; DB 6; Length 402; 24.2%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 402;
                                                                                                                                                                                                                                                                                                                       DB 8; Length 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABF81904 standard; protein; 402 AA.
Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294
WQ200261087-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7;
                                                                                                                                                                                                                                     US-05-2003.
04-DEC-2003.
(DECO-) DECODE GENETICS EHF.
5.9%; Score 70.5; D
ery Match
5.9%; Pred. No. 51;
                                                              5.9%; Score 70.5; 1
24.2%; Pred. No. 51;
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24.2%; Pred. No. 52;
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24.2%; Pred. No. 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE38522 standard; protein; 402 AA.
Human PTGER3 protein isoform, EP3-V.
WO2003064471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW57410 standard; protein; 402 AA.
Human BP3-V receptor.
JP10113185-A.
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Human GPCR PTGER3, SEQ ID NO:722.
WO2004040000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE38514 standard; protein; 407 AA.
Human PTGER3 protein isoform, EP3g.
WO2003064471-A2.
07-AUG-2003.
                                                                                                                                                          ADI35081 standard; protein; 393 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 393 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-AUG-2002.
(LIFE-) LIFESPAN BIOSCIENCES INC.
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04-DEC-2003.

(DECO-) DECODE GENETICS EHF.

6ry Match 5.9%;

6ry Match 7:milarity 24.2%;
07-AUG-2003.
(DECO-) DECODE GENETICS EHF.
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(ONOY ) ONO PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-2004.
(VAND-) VAN ANDEL INST.
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Best Local Similarity
RESULT 1091
                                                                 Query Match
Best Local Similarity
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RESULT 1092
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Best Local Similarity
RESULT 1095
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RESULT 1096
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(PRIM-) PRIMAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                               ADI35073 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-2003
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ABP40525 standard; protein; 499 AA.
Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.
                                                                                   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2. US2003224393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3 US2003224393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                       ADI35071 standard; protein; 425 AA.
Human prostaglandin E receptor subtype EP3 (PTGER3) protein
US2003224393-A1.
5.9%; Score 70.5; DB 7; Length 407; 24.2%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 425;
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                                                                                                                                                                              Length 407
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Wheat sugar transport protein encoded by wlk8.pk0001.all.
US6383776-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU30473 standard; protein; 521 AA.
Protein encoded by Prokaryotic essential gene #16000
WO200277183-A2.
                                                                                                                      USACCE-2003.
04-DEC-2003.
(DECO-) DECODE GENETICS EHF.
5.9%; Score 70.5; DB 8;
ery Match 5.9%; Pred. No. 53;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INWR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS. (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O4-DEC-2003.
(DECO-) DECODE GENETICS EHF.
(DECO-) DECODE GENETICS EHF.
5.9%; Score 70.5; DB
(ery Match anilarity 24.2%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 30-APR-2002.

PA (GENO-) GENOME THERAPEUTICS CORP.

QUETY MATCh 5.9%; Score 70.5; DB
BEST Local Similarity 20.5%; Pred. No. 71;
RESULT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70.5; DB
Pred. No. 75;
                                                                                                                                                                                                                                                                                                              PD 07-AUG-2003.

PA (DECO-) DECODE GENETICS EHF.

Query Match 5.9%; Score 70.5; I
Best Local Similarity 24.2%; Pred. No. 57;
RESULT 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 07-AUG-2003.

PA (DECO-) DECODE GENETICS EHF.

Query Match

S.9*; Score 70.5; I

Best Local Similarity 24.2*; Pred. No. 58;

RESULT 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.9%; Score 70.5; 1
24.2%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%; Score 70.5; 23.1%; Pred. No. 67;
                                                                                                                                                                                                                                           AAE38518 standard; protein; 425 AA.
Human PTGER3 protein isoform, EP3f.
WO2003064471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE38515 standard; protein; 433 AA.
Human PTGER3 protein isoform, EP3h.
WO2003064471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW98431 standard; protein; 480 AA.
H. pylori GHPO 446 protein.
WGO843478-Al.
WG-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 433 AA
                                                                   protein; 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2003.
(DECO-) DECODE GENETICS EHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
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Length 717;

Length 740;

Length 766;

us-10-063-518-14.rag.spdi

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Query Match 5.9%; Score 70.5; DB 8; Length 1147; Best Local Similarity 19.5%; Pred. No. 2.2e+02; RESULT 1124
Human prostate cancer antigen protein sequence SEQ ID NO:1299 WO200055174-A1.
21-SEP-2000.
                                                                                                                                                                                                                                                                                                                     AAG39555 standard; protein; 766 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 48959.
BP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG39554 standard; protein; 815 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 48958.
EP1033405-A2.
66-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG39553 standard; protein; 927 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 48957.
BP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUH22510 standard, protein, 1147 AA.

Human transporter & ion channel (TRICH) protein SeqID8
W02003444-A2.
                                                                                                                                                             ADG47941 standard; protein; 740 AA.
Arabidopsis thaliana-like sugar transport protein #2.
26-DEC-2002.
(HELENTJARIS T G.
(HELEN) HELENTJARIS T G.
5.9%; Score 70.5; DB 8; Lengert Local Similarity 22.8%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP73754 standard; protein; 1026 AA.
Candida albicans essential protein SEQ ID NO 7591.
WO200253728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-ULL-2002.
(ELIT-) ELITRA PHARM INC.
S.9%; Score 70.5; DB 5;
Hery Match 5.9%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-1997.

(CHEM-) CHEMGENICS PHARM INC.

(CHEM-) CHEMGENICS PHARM INC.

5.9%; Score 70.5; DB 2;

lery Match 5.9%; Pred. No. 1.98+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70.5; DB 7;
Pred. No. 2.3e+02;
                                                                                                     5.9%; Score 70.5; DB 3; 22.4%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                      wuery Match
Best Local Similarity 21.3%; Pred. No. 1.38+02;
RESULT 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.9%; Score 70.5; DB 3; 21.3%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.9%; Score 70.5; DB 3; 21.3%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 22.3%; pred. No. RESULT 1122

ID AAM17057 standard; protein; 1027 AA.

DE Candida albicans chitin synthase (CHSI).

PN W09716549-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADKI8350 standard; protein; 1163 AA.
Human NOVX protein #2.
WO2003057854-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM29274 standard; protein; 1163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 19.5%;
RESULT 1125
                                                                (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human novel protein NOV2b. WO2003064628-A2. 07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-NOV-2003.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1121
                                                                                                                         Best Local Similarity RESULT 1117
                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2003.
(SYNA-) SYNAPTIC PHARM CORP.
6ry Match 5.9%; Score 70.5; DB 7; Length 599;
cry Match 5.9%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 662;
                                                                                                                                                                                                                                                DB 6; Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.9%; Score 70.5; DB 6; Length 548; 24.0%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 600;
                                DB 5; Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ64315 standard; protein; 662 AA.
Cartilage differentiation inhibiting protein, SEQ ID 10.
WO2004013326-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wheat Beta-vulgaris-like sugar transport protein #1.
US2002199217-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABW02687 standard; protein; 599 AA.
Rattus norvegicus neuronal GABA transporter (GAT-1)
US2003143729-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 70.5; DB 5;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%; Score 70.5; DB 8; 22.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                        .,
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB92892 standard; protein; 700 AA.
Herbicidally active polypeptide SEQ ID NO 2103.
WO200210210-A2.
                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                      Score 70.5; D
Pred. No. 79;
            (DUPO ) DU PONT DE NEMOURS & CO E I.
5.9%; Score 70.5; I
st Local Similarity 26.0%; Pred. No. 79;
                                                                                                                                                                                                                                                Score 70.5; I
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%; Score 70.5; 1
19.5%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 70.5; 20.1%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD46023 standard; protein; 599 AA.
Rat Protein P23978, SEQ ID NO 11695.
W02003016475-A2.
27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1116
ID AAB56721 standard; protein; 717 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM78767 standard; protein; 600 AA.
Human protein SEQ ID NO 1429.
WO200157190-A2.
                                                                                      ABU08338 standard; protein; 539 AA. Wheat sugar transport protein #4. US2002178468-A1.
                                                                                                                                                                                                                                                                                                           ADG47930 standard; protein; 539 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%;
                                                                                                                                                                                                                                                5.9%;
                                                                                                                                                                                                                                                                                                                                                       PD 26-DEC-2002.
PA (HELE/) HELENTJARIS T G.
Query March 5.9%;
Best Local Similarity 26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002
(ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-2004.
(ASAH ) ASAHI KASEI KK.
                                                                                                                                                                 (ALLE) ALLEN S M.
(HITZ/) HITZ W D.
(KINN/) KINNEY A J.
(TING/) TINGEY S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1112
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                Best Local Similarity RESULT 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FARB ) BAYER AG.
                                                                                                                                                   28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                    Query Match
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Length 1026;

Length 927;

Length 815;

Length 1027;

BERE

Length 1163;

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PD 21-APR-1998.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Watch
5.9%; Score 70.5; DB 2; Length 1780;
Best Local Similarity 34.8%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E Angiogenesis-associated human protein sequence #22.

N W0200279492-A2.

D 10-0CT-2002.

A (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match

Best Local Similarity 34.8%; Pred. No. 4.1e+02;
    Query Match 5.9%; Score 70.5; DB 7; Length 1163; Best Local Similarity 19.5%; Pred. No. 2.3e+02; RESULT 1126
                                                                                                                                                                                                                                                                                                             PD 18-JUL-2000.

PA (UYOR-) UNIV OREGON HEALTH SCI.

Query Match 5.9%; Score 70.5; DB 3; Length 1780;

BBSt Local Similarity 34.8%; Pred. No. 4.1e+02;

RESULT 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%; Score 70.5; DB 5; Length 1783; 34.8%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%; Score 70.5; DB 4; Length 1795; 34.8%; Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 2; Length 225;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 70; DB 3; Length 189; 26.2%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%; Score 70; DB 3; Length 185; 26.2%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG34242 standard; protein; 185 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 41631.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG34241 standard; protein; 189 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 41630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW44944 standard; protein; 225 AA.
Avian infectious bronchitis virus glycoprotein M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 34.8%; Pred. No. 4.1e+02;
RESULT 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG21018 standard; protein; 1795 AA.

E Novel human diagnostic protein #21009.

N W0200175067-A2.

11-OCT-2001.

A (HYSE-) HYSEQ INC.

Guery Match

Best Local Similarity 34.8%; Pred. No.
                                                                             AAW53863 standard; peptide; 1780 AA.
Human gravin polypeptide.
US5741890-A.
                                                                                                                                                                                                                                        AAB15380 standard; protein; 1780 AA. Human gravin protein sequence. US6090929-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB97448 standard; protein; 1783 AA.
Novel human protein SEQ ID NO: 716.
WO200222660-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   AA017365 standard; protein; 1781 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU03477 standard; protein; 1781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-1998.
(INMR ) RHONE MERIEUX SA.
Query Match
Similarity 21.6%;
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2002.
(SCHD ) SCHERING AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gravin.
EP1191107-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     PPRED
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Ouery Match 5.9%; Score 70; DB 3; Length 287; Best Local Similarity 26.0%; Pred. No. 38; RESULT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query March
Best Local Similarity 26.2%; Pred. No. 41;
RESULT 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          II.MAY-1995.
(ALCO-) ALCOHOLISM & DRUG ADDICTION RES FOUND.
5.9%; Score 70; DB 2; Length 333;
ery Match 5.9%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vuery Match 5.9%; Score 70; DB 3; Length 333; Best Local Similarity 23.6%; Pred. No. 46;
                                                                                                                                                                                                                                                                            5.9%; Score 70; DB 3; Length 235; 26.2%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%; Score 70; DB 4; Length 256; 20.2%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.9%; Score 70; DB 3; Length 274; Best Local Similarity 26.0%; Pred. No. 35; RESULT 1139
                                                                                                                    Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG53762 standard; protein; 274 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 68478.
EP1033405-A2.
                                                                                                                                                                        -A-3-340 standard; protein; 235 AA.
Aradidopsis thaliana protein fragment SEQ ID NO: 41629.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG53761 standard; protein; 287 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 68477.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY90647 standard; protein; 333 AA.
Human mutant G protein-coupled receptor GPR8 (T259K).
WO200022129-A1.
ADB09893 standard; protein; 226 AA.
Alloicoccus otitis antigenic protein SEQ ID NO:3730.
W02003048304-A2.
(AMMP) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABÜJS677 standard; protein; 292 AA.
Protein encoded by Prokaryotic essential gene #21204
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                       ABB69790 standard; protein; 256 AA.
Drosophila melanogaster polypeptide SEQ ID NO 36162.
WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK48488 standard; protein; 307 AA.
Streptococcus pneumoniae protein, Seq ID No 5003.
US6699703-B1.
                                                                                                                  5.9%; Score 70; DB 6; 24.1%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 22.5%; Pred. No. 38;
RESULT 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY90613 standard; protein; 333 AA.
Human G protein-coupled receptor GPRB.
WO200022129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR72985 standard; protein; 333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epsilon opioid receptor. W09512670-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1138
                                                                                                                                  Best Local Similarity RESULT 1136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002
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                                                                                                                  Query Match
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Human G protein-coupled receptor GPR8 protein SEQ ID NO:279 WO200261087-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR61545 standard; protein; 333 AA. Human GPR8 receptor polypeptide. WO2003081234-A2. C2-OCT-2003. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH14164 standard; protein; 333 AA.
Mutated human GPR8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC51793 standard; protein; 333 AA.
Human GPR8, SEQ ID 4.
WO2003057236-A1.
                                                                                                                      ARR57245 standard; protein; 333 AA.
Human GPR8 protein SEQ ID NO:84.
WO2003045994-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH14008 standard; protein; 333 AA. Human GPR8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIAW/) LIAW C W.
(BEHA/) BEHAN D P.
(CHAL/) CHALMERS D T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LIAW/) LIAW C W.
(BEHA/) BEHAN D P.
(CHAL/) CHALMERS D T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1161
                                                                      Query Match
Best Local Similarity
RESULT 1154
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                                   Score 70; DB 3; Length 333;
Pred. No. 46;
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                                                                                                                                                                                         Query Match
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 5.9%; Score 70; DB 5; Length 333; Local Similarity 23.6%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                     4; Length 333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Length 333;
                                                                                        AAU01297 standard; protein; 333 AA.
Human G-protein receptor 8, GPR 8, mutant N127A.
W0200127632-A2.
19-APR-2001.
(CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
(WILL/) WILLIAMS K M.
                                                                                                                                                                                                                                                                                                                                                                                                  AAU01298 standard; protein; 333 AA.
Human G-protein receptor 8, GPR 8, mutant T259B.
WO200127632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG65918 standard; protein; 333 AA.
G protein-coupled receptor related peptide #6.
WO200244368-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ37874 standard; protein; 333 AA.
GPR7 ligand related human protein SEQ ID No
WO2002102847-A1.
                                                                                                                                                                                                                                                                                                                                                       DB
46;
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46;
                                                                                                                                                                                                                                                                                                                                                   Query Match 5.9%; Score 70; Best Local Similarity 23.6%; Pred. No. RESULT 1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB84683 standard; protein; 333 AA.
Human GPR8-ligand related protein #1.
27-02010 98494-A1.
27-DEC-2001.
GTAKE) TAKEDA CHEM IND LTD.
5.9%; Score 70;
EL Local Similarity 23.6%; Pred. No.
                                                                                                                                                                                                                                                AAU01295 standard; protein; 333 AA.
Human G-protein receptor 8, GPR 8.
W0200127632-A2.
(CAAR-) CAMBRIDGE DRUG DISCOVERY LTD.
(WILL/) WILLIAMS K M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-APR-2001.
(CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
(WILL/) WILLIAMS K M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB84723 standard, protein; 333 AA. Human GPR8-ligand related protein #3. WO200198494-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU61448 standard; protein; 333 AA.
Screening method related protein #1.
W0200293161-A1.
(TAKE) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP81897 standard; protein; 333 AA.
                                   5.9%;
Local Similarity 23.6%;
1145
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(TAKE ) TAKEDA CHEM IND LTD.
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(TAKE ) TAKEDA CHEM IND LTD.
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(TAKE ) TAKEDA CHEM IND LTD.
        20-APR-2000.
(AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1148
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Best Local Similarity
RESULT 1149
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Best Local Similarity
RESULT 1152
                                         Query Match
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RESULT 1150
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T7-JUL-2003.
(TAKE) TAKEDA CHEM IND LTD.
ery Match
S.9%; Score 70; DB 7; Length 333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.9%; Score 70; DB 7; Length 333;
                                                                                                                                                                                            DB 7; Length 333; 46;
                                                                                                                                                                                                                                         DE PAC22691 standard; protein; 333 AA.

DE Human G protein-coupled receptor (GPCR) polypeptide #44.

DE Human G protein-coupled receptor (GPCR) polypeptide #44.

DE 29-APR-2003.

Query Match Similarity 23.6%; Score 70; DB 7; Length 333;

RESULT 1156

DE Human G protein-coupled receptor (GPCR) polypeptide #5.

DE Human G protein-coupled receptor (GPCR) polypeptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7; Length 333; 46;
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                                       Length 333,
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23.6%; Pred. No. 46;
                                       DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 23.6%; Pred. No. RESULT 1160
                                                                                                                                                          PD 05-JUN-2003.

PA (TAKE) TAKEDA CHEM IND LTD.
QUETY MATCh 5.9%; Score 70;
Best Local Similarity 23.6%; Pred. No. 4
(LIFE-) LIFESPAN BIOSCIENCES INC.
(LIFE-) MATCH
5.9%; Score 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%; Score 70; 23.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duery Match
Best Local Similarity 23.6%; Score 70
RESULT 1159
ID ADG41976 standard; protein; 333 AA.
DB Huan GPR8 polypeptide.
PN JP2003009867-A.
PD 14-JAN 2003.
PA (TAKE) TAKEDA CHEM IND LITD.
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5.9%; Score 70; DB 8; Length 388; 24.8%; Pred. No. 57;
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                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 70; DB 8; Length 388; 24.8%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 70; DB 6; Length 399; 22.9%; Pred. No. 59;
                     Score 70; DB 8; Length 378;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 22.9%; Score 70; DB 6; Length 47
RESULT 1178
DB ABLE/878 standard; protein; 475 AA.
DB Human transporter and ion channel-24 (TRICH-24) protein.
PD 06-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.9%; Score 70; DB 6; Beet Local Similarity 22.9%; Pred. No. 59; RESULT 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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Photorhabdus luminescens protein sequence #361
WO200294867-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB Best Local Similarity 25.9%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAY-2003.
(GENO-) GENOME THERAPEUTICS CORP.
5.9%; Score 70; DB
tery Match
7.1.1 Similarity 23.5%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC96947 standard; protein; 425 AA.
B. faecium protein sequence SEQ ID 6574.
US6583275-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA34110 standard; protein; 470 AA. Acinetobacter baumannii protein #1271. US6562958-B1.
                                                                                                                                                                                                                                                                                                      ADO29591 standard; protein; 388 AA. Mouse GPCR OXTR, SEQ ID NO:693. WO2004040000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA54410 standard; protein; 399 AA.
Human protein, SEQ ID 1978.
EP1293569-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG99947 standard; protein; 399 AA.
Human novel polypeptide #60.
WO200274961-Al.
                                                                             protein; 388 AA.
                                                                                                  Mouse oxytocin receptor protein. US2004086881-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
              Best Local Similarity 23.6%;
RESULT 1171
  (NORA-) NORAK BIOSCI INC.
                                                                                                                                                         (RAMA/) RAMANATHAN C S. (GOPA/) GOPAL S.
                                                                                                                                                                                (GOPA/) GOPAL S.
(MINT/) MINTIER G A.
(FEDE/) FEDER J.
                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1177
                                                                                                                                                                                                                                                                                                                                                              13-MAY-2004.
(PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2002.
(HYSE-) HYSEQ INC.
                                                                               ADN49121 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-2002
                                                                                                                                          06-MAY-2004
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG12858 standard; protein; 378 AA.
MA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.
WO2003097795-A2.
27-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADGI2854 standard; protein; 347 AA.
Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.
WO2003097795-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG12856 standard; protein; 364 AA.
Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.
WO2003097795-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.

DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.

PN WO2004048938-A2.

PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match

Best Local Similarity 23.6%; Pred. No. 46;

RESULT 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%; Score 70; DB 5; Length 364; 25.0%; Pred. No. 52;
                                                                                                                                        ; DB 8; Length 333;
. 46;
                                                                                                                                                                                                                                                                                                      5.9%; Score 70; DB 8; Length 333; 23.6%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 333;
46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%; Score 70; DB 8; Length 347; 23.6%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70; DB 8; Length 364;
Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%; Score 70; DB 8; Length 364, 23.6%; Pred. No. 52;
                                     ADG12852 standard; protein; 333 AA.
Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.
WO2003097795-A2.
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.9%; Score 70; Best Local Similarity 23.6%; Pred. No. RESULT 1165
                                                                                    WOLULO.
27-NOV-2003.
(NORA-) NORAK BIOSCI INC.
(NORA-) MORAK BIOSCI INC.
5-9%; SCOIE 70;
lery Match 23.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                      Human GPR8 protein; 333 AA. WOZO04041301-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG30839 standard; protein; 364 AA.
Human calcium channel protein.
WO200252003-A2.
                                                                                                                                                                                               ADD29700 standard, protein; 333 AA. Human GPCR GPR8, SEQ ID NO:802. MOZO04040000-A2. [BAY-2004. (PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO28778 standard; protein; 364 AA.
Human GPR8-enhanced receptor.
US2004091946-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%;
23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-2004.
(TAKE) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-2003.
(NORA-) NORAK BIOSCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-2003.
(NORA-) NORAK BIOSCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAY-2004.
(OAKL) OAKLEY R H.
(BARA) BARAK L S.
(LAPO) LAPORTE S A.
(CARO) CARON M G.
                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 1164
                                                                                                                                                         Best Local Similarity
RESULT 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  T 1164
ADO31044 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUL-2002.
(FARB ) BAYER AG.
                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1168
                                                                                                                                                                                                                                                                                                                                                                   PPREE
```

Length 399;

Length 470;

Length 474;

ADP07803 standard; protein; 138 AA. Human secreted protein, seg id 286. WO2004042000-A2.

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WCZUCZOO.
WCEN-2000.
(MICR-) MICROBIAL TECHNICS LTD.
(MICR-) MICROBIAL TECHNICS LTD.
5.9%; Score 70; DB 3; Length 640;
ery Match
5.9%; Score 70; DB 3; Length 640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-2004.

06-JAN-2004.

(GENO-) GENOME THERAPEUTICS CORP.

6-TY Match 5.9%; Score 70; DB 8; Length 767;

ery Match 5.9%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB 2; Length 980; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%; Score 70; DB 4; Length 552; 25.0%; Pred. No. 93;
                                                                                                       Length 506;
                                                                                                                                                                                                                                       DB 6; Length 506;
82;
                                                                                                                                                                                                                                                                                                                                                                          ; DB 5; Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 637,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             July 13453 standard; protein; 637 AA.
Protein encoded by Prokaryotic essential gene #18980.
W020027183-A2.
(BLIT-) ELITRÀ PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY91335 standard; protein; 640 AA.
Group B Streptococcus protein sequence SEQ ID NO:68.
WO200006736-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU18262 standard; protein; 602 AA.
Protein encoded by Prokaryotic essential gene #3789
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AARS3921 standard; protein; 980 AA.
HCV fusion protein corresp. to N-terminal of ORF.
JP06092996-A.
(SHIM/) SHIMOTOYA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.9%; Score 70; DB 6; 1
Best Local Similarity 23.1%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WOZOT-2002.
03-0CT-2002.
(ELIT-) ELITRA PHARM INC.
5.9%; Score 70; DB 6;
lery Match 5.9%; Pred. No. 1e+02;
                                                                                                     Score 70; DB 6;
Pred. No. 82;
ADA89683 standard; protein; 506 AA.
Staphylococcus aureus antigenic protein #222.
WO2003011899-A2.
                                                                                                                                                                                                                                         Score 70;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                            Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 25.0%; Pred. 1
RESULT 1182
ID AAM39017 standard; protein; 552 AA.
Be Human polypeptide SEQ ID NO 2162.
PN W020012312-Al.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
                                                                                                                                                        ABM72414 standard; protein; 506 AA. Staphylococcus aureus protein #1654 WO200294868-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL04660 standard; protein; 767 AA. A. catarrhalis protein #426. US6673910-B1.
                                                                                                                                                                                                                                                                                   AAE21176 standard; protein; 540 AA. Human TRICH-20 protein. WO200212340-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%;
                                                                                                       5.9%;
                                                                                                                                                                                                                                            5.9%;
                                                                                                                                                                                                                                                                                                                                                                            5.9%;
                                                                                                                                                                                                                                                                                                                                              14-FEB-2002.
(INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000.
2000.
2000.
2R-) MICROBIAL TE.
2ry Match
Best Local Similarity 21
RESULT 1186
ID ADL04660 standar
DE M. catarrhal
PD US66739**
                                                  13-FEB-2003.
(UYSH-) UNIV SHEFFIELD.
(BIOS-) BIOSYNEXUS INC.
                                                                                                                                                                                                PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 2
RESULT 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 1187
                                                                                                       Query Match
Best Local Similarity
RESULT 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
RESULT 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1183
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PN DE
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AAU01288 standard; protein; 218 AA.
Brassica napus fatty acid desaturase, Fad3C, mutant partial sequence.
WO200125453-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 12-APR-2001.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 5.8%; Score 69.5; DB 4; Length 218;
Best Local Similarity 29.3%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 69.5; DB 4; Length 261; 27.7%; Pred. No. 38;
                                                                                                                                                          PD 13-MAY-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match
3.8 strong Score 69.5; DB 6; Length 198;

Best Local Similarity 23.3 strong No. 26;

RESULT 1190

ADB09276 standard; protein; 201 AA.

DE Alloicoccus oritis antigenic protein SEQ ID NO.3216.

PN WO2003048304-A2.

PD 12-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CO-SEP-2001.
(PHAA ) PHARMACIA & UPJOHN CO.
(PHAA ) PHARMACIA & UPJOHN CO.
(ST. Match 5.8%; Score 69.5; DB 4; Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 247;
21-MAY-2004.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.8%; Score 69.5; DB 8; Length 138;
-- rocal Similarity 22.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                        Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                  _AAU329449 standard; protein; 210 AA.
Human G protein-coupled receptor (GPCR) polypeptide #70.
WO200168858-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MBG66935 standard; protein; 253 AA.
Novel G-protein coupled receptor related protein #12.
WO200240539-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB62542 standard; protein; 261 AA.
Drosophila melanogaster polypeptide SEQ ID NO 14418.
WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                                        5.8%; Score 69.5; DB 6; 26.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGE60737 standard; protein; 210 AA.
Novel G protein coupled receptor (nGCPR-x) #70.
US2002058306-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vuery Match 5.8%; Score 69.5; I Best Local Similarity 26.0%; Pred. No. 35; RESULT 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.8%; Score 69.5; I
24.2%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 69.5; I
20.9%; Pred. No. 28;
                                                                                  Acinetobacter baumannii protein #825.
186562958-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO80446 standard; protein; 270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUN-2003.
(AMHP ) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                                                                                          (AMHP ) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1197
                                           Query Match
Best Local Similarity
RESULT 1189
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
RESULT 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-2002.
(VOGE/) VOGELI G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                Query Match
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ABW02126 standard; protein; 308 AA.
Human GPCR3 protein.
US2003195335-A1.
                                                                                                           CASMAN S.
ALSOBROOK J P.
BURGESS C E.
PADIGARU M.
                                                                                                                                                                                                                                                                                                                                                    (MACD/) MACDOUGALL J R.
                                                                                                                                                                                                                                                     SHENOY S.
KEKUDA R.
GANGOLLI E A.
STONE D J.
SMITHSON G.
                                                                                                                                                                                   TAYLOR S.
TCHERNEV V T.
SPYTEK K A.
                                                                       GROSSE W M.
SZEKERES E S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
RESULT 1208
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-1999.
(GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                               (GANG/)
(STON/)
(SMIT/)
                                                                                                                                                                                                                                      (LILL/)
(SHEN/)
(KEKU/)
                                                                                                           (CASM/)
                                                                                                                              (ALSO/)
(BURG/)
                                                                                                                                                                                   (TAYL/)
(TCHE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU95729 standard; protein; 308 AA.
Human olfactory and pheromone G protein-coupled receptor #216.
WO200224726-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.8%; Score 69.5; DB 7; Length 308;
Best Local Similarity 20.9%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.8%; Score 69.5; DB 4; Length 308; 20.9%; Pred. No. 47;
                                                                         Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8%; Score 69.5; DB 5; Length 308; 20.9%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8%; Score 69.5; DB 5; Length 308; 20.9%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 69.5; DB 5; Length 308; 20.9%; Pred. No. 47;
                                                                                                                                                                                                                         DB 7; Length 296;
                                                                                                                                                                                                                                                                          AAG71524 standard; protein; 308 AA.
Human olfactory receptor polypeptide, SEQ ID NO: 1205.
WO20127158-A2.
19-APR-2001
                                                                           DB 7;
                                                                                                                        ADE86076 standard; protein; 296 AA.
Streptomyces hygroscopicus ABC transporter.
WO2003082909-A1.
                                                    (GENO-) GENOME THERAPEUTICS CORP.

17 Match
18 Local Similarity 22.1%; Pred. No. 40;
                                                                                                                                                                                                                         5.8%; Score 69.5; 1
21.0%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                        5.8%; Score 69.5; I
20.9%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%; Score 69.5; I
20.9%; Pred. No. 47;
   Pseudomonas aeruginosa polypeptide #12621.
US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP55703 standard; protein; 308 AA. Human GPCR polypeptide SEQ ID NO 216. WO200216548-2002. RFEB-2002. (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB44525 standard; protein; 308 AA. Human GPCR3 polypeptide SEQ ID NO 9. WO200174904-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC86333 standard; protein; 308 AA. Human GPCR protein SEQ ID NO:786. EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU85362 standard; protein; 308 AA. G-coupled olfactory receptor #223., WO200198526-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1201
ID AAU24742 standard; protein; 308 AA.
DE Human olfactory receptor AOLFR242.
PN WO200168805-A2.
                                                                                                                                                                                                                                                                                                                                                    (VEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2001.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                    Best Local Similarity RESULT 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-DEC-2001.
(SENO-) SENOMYX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SENO-) SENOMYX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2002.
(CHEM-) CHEMCOM SA.
                                                                           Query Match
Best Local Similarity
RESULT 1198
                                                                                                                                                                                   09-OCT-2003.
(AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                           Query Match
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ABM49658 standard; protein; 327 AA.
Propionibacterium acnes predicted ORF-encoded polypeptide #14334
WO2003033515-A1.
24-APR-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.8%; Score 69.5; DB 7; Length 321; Best Local Similarity 18.8%; Pred. No. 50; RESULT 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69.5; DB 6; Length 327;
Pred. No. 52;
DB 7; Length 308;
                                                                                                                                                   DB 6; Length 316;
                                                                                                                                                                                                                                                                                                5.8%; Score 69.5; DB 2; Length 321; 21.4%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 327
                                                                                                                                                                                                       AAY35360 standard; protein; 321 AA.
Chlamydia pneumoniae involved in the virulence process
WO9927105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU53139 standard; protein; 327 AA.
Propionibacterium acnes immunogenic protein #14035.
WO200181581-A2.
                                                      ABR01671 standard; protein; 316 AA.
Human G protein coupled receptor SEQ ID 202.
WO2003000735-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH10684 standard; protein; 354 AA.
Rat Sprague-Dawley putative GCR polypeptide.
5.8%; Score 69.5; C 20.9%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.8%; Score 69.5; 1
Best Local Similarity 25.5%; Pred. No. 52;
RESULT 1212
                                                                                                                                                   5.8%; Score 69.5; I
20.9%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                         ADC33485 standard; protein; 321 AA.
Yeast ARV1.
US6566512-B1.
                                                                                                            03-JAN-2003.
(DECO-) DECODE GENETICS EHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%;
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(PEKE ) PE CORP NY.
27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .T 1221
ADLIDES standard; protein; 415 AA.
ADLIDESOSPIAS dmTrplalt2 protein.
W02003002137-A2.
09-JAN-2003.
(DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
5 R$: Score 69.5; DB 7; Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 415;
                                                                                                                                                                               PA (LXRB-) LXR BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 20.2%; Pred. No. 64;
RESULT 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.

TY Match

5.8%; Score 69.5; DB 7; Length 401;
                                                       DB 8; Length 354;
                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 69.5; DB 4; Length 382; 20.2%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU32698 standard; protein; 400 AA.
Protein encoded by Prokaryotic essential gene #18225.
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB66992 standard, protein, 428 AA.
Drosophila melanogaster polypeptide SEQ ID NO 27768.
WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB60948 standard; protein; 415 AA.
Drosophila melanogaster polypeptide SEQ ID NO 9636.
WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                       Human lysophosphatidic acid (LPA) receptor EDG-1.
19548922-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                      ANUO0302 standard; protein; 382 AA.
LPA receptor-related amino acid sequence #1.
W0200112838-A2.
22-FEB-2001.
(ATAI-) ATAIRGIN TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 69.5; I
20.9%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 69.5; 1
20.9%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%; Score 69.5; 20.9%; Pred. No. 72;
                                                   5.8%; Score 69.5; I 22.0%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 69.5; 1
20.2%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69.5;
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69.5; |
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB47613 standard; protein; 400 AA.
Listeria monocytogenes protein #317
WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL12060 standard; protein; 401 AA.
Drosophila dmTrpl protein.
WO2003002137-A2.
                                                                                                        AAYO5489 standard; protein; 382 AA.
Human EDG-2 protein sequence.
WO9919513-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-2002.
(ATAI-) ATAIRGIN TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2002.
(ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                2001.
2001.
AI-) ATAIRGIN TEC.
AI-) ATAIRGIN TEC.
AI-) ATAIRGIN TEC.
AI-) ATAIRGIN TEC.
Best Local Similarity 2.
RESULT 1216
ID ABG76099 standar
DE Human 1980r
PD 26-7
                                    (META-) METABOLEX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2001.
(INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
   WO2003104484-A1.
                                                                                                                                                                    22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2003
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                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1221
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Fusion protein containing rabbit prostaglandin E2EP3 receptor W09953033-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 453;
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                            Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 494;
5.8%; Score 69.5; DB 4; Length 428; 20.9%; Pred. No. 75;
                                                                                                                                                         Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 453;
                                                                                                                                                                                                                                                                                                                                                                  AAG30875 standard; protein; 453 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 36988.
EP1033405-A2.
06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG30874 standard; protein; 476 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 36987.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG30873 standard; protein; 503 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 36986
EP1033405-A2.
6-SEP-2000.
                                                                                                                                                                                                       09-JAN-2003.
(DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK47327 standard; protein; 453 AA.
Streptococcus pneumoniae protein, Seq ID No 3842.
US6699703-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2004.
(GENO-) GENOME THERAPEUTICS CORP.
(ery Match 5.8%; Score 69.5; DB 8;
ery Match 24.4%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7;
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                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABOGIG37 standard; protein; 494 AA.
Tebsiella pneumoniae polypeptide segid 8154.
US6610836-B1.
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(GENO-) GENOME THERAPEUTICS CORP.
5.8%; Score 69.5; D
erry Match
5.8%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 69.5; I 23.6%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.8%; Score 69.5; 1
23.3%; Pred. No. 94;
                                                                                                                                           wery match 5.8%; Score 69.5; Best Local Similarity 20.9%; Pred. No. 75; RESULT 1224
                                                                                                                                                                                                                                                                                                        Score 69.5; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 69.5; 1
23.3%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY92829 standard; protein; 535 AA.
C. pneumoniae CPN100557 processed antigen.
WO200024765-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 22.0%; Pred. 1
RESULT 1229
ID AAY41278 standard; protein; 500 AA.
                                                         ADL12058 standard; protein; 428 AA.
Drosophila dmTrplalt1 protein.
WO2003002137-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WOLVOLL
04-MAY-2000.
(CONN-) CONNAUGHT LAB LTD.
(CONN ALCh 5.8%;
                                                                                                                                                                                                                                                                      PD 21-OCT-1999.

PA (UYVA-) UNIV VANDERBILT.

QUETY MATCh 5.8%;

Best Local Similarity 23.6%;

RESULT 1225
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Best Local Similarity
RESULT 1227
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Best Local Similarity
RESULT 1228
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Best Local Similarity
RESULT 1230
   Query Match
Best Local Similarity
RESULT 1223
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Best Local Similarity
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ABBB2979 standard; protein; 557 AA.
Human SLC22A related protein-GenBank Identifier No. GI# 3242598
WO200299053-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB2980 standard; protein; 557 AA.
Human SLC22A related protein-GenBank Identifier No. GI# 4507005
WO200299053-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.9%; Score 69.5; DB 6; Length 557; Best Local Similarity 26.3%; Pred. No. 1.1e+02; RESULT 1239
                                                                                                     Score 69.5; DB 3; Length 547; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69.5; DB 6; Length 557; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                    Length 547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 557
                                                                                                                                                      AB0226764 standard; protein; 547 AA.
Protein encoded by Prokaryotic essential gene #12291.
W0200277183-A2.
                                                                                                                                                                                                                                                                                                                             Leary Match
Best Local Similarity 23.6%; Pred. No. 1.1e+02;
RESULT 1235
ID AAY01650 standard; protein; 557 AA.
PN W0991307-2A1.
PD 18-MAR-19an.
PA //...
                                                                                                                                                                                                                                                                                                                           ABU31940 standard; protein; 551 AA.
Protein encoded by Prokaryotic essential gene #17467
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 18-MAR-1999.

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC. Query Match 5.8%; Score 69.5; DB 2; Best Local Similarity 26.3%; Pred. No. 1.1e+02; RESULT 1289.
                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
Query Match
5.8%; Score 69.5; DB 6;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 69.5; DB 3; 26.3%; Pred. No. 1.1e+02;
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26.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-2000.
(CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human carnitine transporter protein OCTN2. W0200014210-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB007242 standard; protein; 557 AA.
Human p53 modifying protein, SEQ ID 202.
WO200299122-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG03029 standard; protein; 557 AA.
Novel human diagnostic protein #3020.
WO200175067-A2.
AAY92828 standard; protein; 547 AA. C. pneumoniae CPN100557 antigen. WO200024765-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%;
                                                                              (CONN-) CONNAUGHT LAB LTD.
ry Match 5.8%;
t Local Similarity 21.4%;
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(EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-2002.
(EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-2002.
(EXEL-) EXELIXIS INC.
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Best Local Similarity
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Best Local Similarity
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                                                                                                   Query Match
Best Local Similarity
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(HYSE-) HYSEQ INC.
                                                               04-MAY-2000
                                                                                                                                                                                                                              03-OCT-2002
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                                                                                                                                             RESULT 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1238
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وال Score 69.5; DB 5; Length 599; Best Local Similarity 19.6%; Pred. No. 1.2e+02; RESULT 1250
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                                                                                                        Length 557;
                                                                                                                                                                                                                                                                           Length 557;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 579;
ADE09321 standard; protein; 557 AA.
Novel protein-related contig polypeptide sequence #387, w02003054152-A2.
03-JUL-2003.
(HYSE-) HYSEQ INC.
                                                                                                                                                            ADE09261 standard; protein; 557 AA.

Novel protein related contig polypeptide sequence #327.
W02003054152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 03-CCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match

BEST Local Similarity 21.1%; Pred. No. 1.1e+02;

RESULT 1240
                                                                                                                                                                                                                                                                                                                                                                                        PD 13-MMY-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.

QUESTY MATCh

Best Local Similarity 20.2%; Pred. No. 1.1e+02;

RESULT 1240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vuery Match 5.8%; Score 69.5; DB 5; Best Local Similarity 22.4%; Pred. No. 1.1e+02; RESULT 1246
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(HELI) HELIX RES INST.
(REAL-) RES ASSOC BIOTECHNOLOGY.

FRY Match

TY Match

Transl Similarity 22.7%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vuery Match 5.8%; Score 69.5; DB 5;
Best Local Similarity 21.1%; Pred. No. 1.1e+02;
RESULT 1248
                                                                                                        5.8%; Score 69.5; DB 7; 26.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-2003.

(GENO-) GENOME THERAPEUTICS CORP.

Query March

Best Local Similarity 23.6%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                         5.8%; Score 69.5; DB 7; 26.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABO62908 standard; protein; 564 AA.
Klebsiella pneumoniae polypeptide seqid 9425.
US6610836-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB65515 standard; protein; 573 AA.
Human protein encoded by clone TEST120271790.
EP1308459-A2.
                                                                                                                                                                                                                                                                                                                                   ADA34637 standard; protein; 559 AA. Acinetobacter baumannii protein #1798. US6562958-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB47410 standard; protein; 579 AA.
Listeria monocytogenes protein #114.
WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABBB9665 standard; protein; 568 AA.
Human polypeptide SEQ ID NO 2041.
WO200190304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP65234 standard; protein; 599 AA.
Hypoxia-regulated protein #108.
WO200246465-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-2002.
(OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2001.
(INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1247
                                                                                                                     Best Local Similarity RESULT 1242
                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1243
                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-2003
                                                                                                                                                                                                                                                                           Query Match
                                                                                                        Match
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Query Match
                                                                                                                                                Query Match
ABP40194 standard; protein; 660 AA.
Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039
US6380370-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGÉMAY-1999.
(INCY-) INCYIE PHARM INC.
6ry Match
5.8%; Score 69.5; DB 2; Length 663;
ery Match
7. c. Similarity 22.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T2-FEB-2004.
(ASAH) ASAHI KASEI KK.
ery Match 5.8%; Score 69.5; DB 8; Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69.5; DB 6; Length 695; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 660;
Best Local Similarity 27.2%; Pred. No. 1.4e+02;
RESULT 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 681;
                                                                                                                                                                                                                                       5.8%; Score 69.5; DB 7; Length 599; 19.6%; Pred. No. 1.2e+02;
                                                                                 Length 599;
                                                                                                                                                                                                                                                                                                                                                                       Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ64317 standard; protein; 663 AA.
Cartilage differentiation inhibiting protein, SEQ ID 12.
WO2004013326-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU41908 standard; protein; 695 AA.
Protein encoded by Prokaryotic essential gene #27435.
WO200277183-A2.
                                                                                                                                                                                                                                                                            T 1252
AAY41285 standard, protein, 656 AA.
A77A-TL fusion protein encoded by plasmid pLJMS-42T
WO9953033-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.8%; Score 69.5; DB 8;
Best Local Similarity 24.5%; Pred. No. 1.4e+02;
RESULT 1258
                                                                                                                                                                                                                                                                                                                               PD 21-OCT-1999.
PA (UYVA-) UNIV VANDERBILT.
Query March
Best Local Similarity 23.6%; Pred. No. 1.4e+02;
RESULT 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 69.5; DB 7; 22.0%; Pred. No. 1.4e+02;
                                                                 MILL-) MILLENNIUM PHARM INC.

ry Match

5.8%; Score 69.5; DB 7;

t Local Similarity 19.6%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY17390 standard; protein; 663 AA.
Human vesicle membrane protein-like protein 3.
WO9921994-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD009827 standard; protein; 681 AA.
Hamster SGLT homologue protein SEQ ID NO:50.
WQ2004039405-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM83092 standard; protein; 663 AA.
Human vesicle membrane protein (VMP)2.
US2003175787-A1.
                                                                                                                                    ADD46025 standard; protein; 599 AA.
Human Protein P30531, SEQ ID NO 11697.
WO2003016475-A2.
 AAE38584 standard; protein; 599 AA.
Human GATI GABA transporter protein.
WO2003061573-A2.
31-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 24.3%;
RESULT 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-2004.
(TAKE) TAKEDA CHEM IND LTD.
                                                                                                                                                                                         27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L999.

Y-) INCYTE PHARN
LY MATCH
Best Local Similarity 2.
RESULT 1255
ID ADM83092 standa-
DE Human vesic'
PD US20031-
PD 18-
PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1257
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1256
                                                                                                                                                                                                                                                                                                           PN
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                                                                                                                                           PACE
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PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match 5.8%; Score 69.5; DB 6; Length 1010;

Best Local Similarity 24.7%; Pred. No. 2.5e+02;

RESULT 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1028;
                                                                                                                                                                                                                                                                                PD 03-0CT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match

Best Local Similarity 19.9%; Pred. No. 1.8e+02;

RESULT 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) 13.JUN-2002.

A (INCY-) INCYTE GENOMICS INC.

S.8%; Score 69.5; DB 5; Length 863;

Dest Local Similarity 19.3%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%; Score 69.5; DB 3; Length 877; 22.7%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 881;
                                                                                                                                                                                                                                                                                                                                                                                       AAY70245 standard; protein; 805 AA.

Human Polycystin-L protein.

W0200012046-A2.

09-MAR-2000.

(BGHM) BRIGHAM & WOMENS HOSPITAL INC.

Query Match

5.8%; Score 69.5; DB 3; Length 805;
                                                                                                                                                                        Length 764;
                                                                                                                                                                                                                              DE S cerevisiae apoptosis associated protein YJL197W.
PN W0200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANSSEN PHARM NV.
5.8%; Score 69.5; DB 4; I
Best Local Similarity 24.4%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-2003.
(GENO-) GENOME THERAPEUTICS CORP.
S.8%; Score 69.5; DB 6;
ery Match
S.8%; Pred. No. 2.5e+02;
                                                                                                                                                                        5.8%; Score 69.5; DB 8; 21.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae OPT protein YPR194C. W0200052162-A2.
ADJ48367 standard; protein; 764 AA.
Maize oil-associated gene protein #26.
US2004025202-A1.
(LAUR/) LAURIE C C.
(RAVA/) RAVANELLO M.
(SAVA/) SAVAGE T.
(LEDE) LEBEAUX J R.
(ROGE/) ROGERS J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA3462 standard; protein; 1028 AA. Acinetobacter baumannii protein #1623. US6562958-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW25671 standard; protein; 1684 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG70761 standard; protein; 881 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB98140 standard; protein; 863 AA.
Human PMMM Incyte ID 7484157CD1.
WO200246383-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000.
(UYTE-) UNIV TENNESSEE RES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
RESULT 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BECK/) BECKER J M.
(HAUS/) HAUSER M.
(DONH/) DONHARDT A.
(BARN/) BARNES D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1264
                                                                                                                                                                                            Best Local Similarity RESULT 1260
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Propionibacterium acnes permease/transporter-related polypeptide #26784.
WO2003033515-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 214;
                                                                                                                                                                                                                                                                                                                                                                                               Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 69; DB 6; Length 350;
                                                                           Length 191;
                                                                                                                                                                                                                                                Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN46858 standard; protein; 239 AA.
Thermococcus kodakaraensis KOD1 protein sequence SeqID736.
WO2004022736-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABM69545 standard; protein; 337 AA.
Photorhabdus luminescens protein sequence #2642.
WO200294867-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luciy match 5.8%; Score 69; DB 8; Best Local Similarity 23.5%; Pred. No. 38; RESULT 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
9
                                                                                                                                                                                                                                              5.8%; Score 69; DB 2; 28.3%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%; Score 69; DB 6; 24.7%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM03849 standard; protein; 214 AA.
Human protein of the invention SEQ ID NO:2534
EP1347046-Al.
                                                                                                                                                                                                                                                                                                  AAB21047 standard; protein; 214 AA.
Human nucleic acid-binding protein, NuABP-51
WO200044900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP58238 standard; protein; 214 AA.
Human ovary-specific O1-236 (NPM2) protein.
WO200288314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DВ
33;
                                                                         5.8%; Score 69; DB 26.6%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.8%; Score 69; DB Best Local Similarity 24.7%; Pred. No. 33; RESULT 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 69; DB 19.8%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 69; 24.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABM72781 standard; protein; 350 AA.
Staphylococcus aureus protein #2021.
WO200294868-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAR-2004.
(NISC-) JAPAN SCI & TECHNOLOGY CORP
                                                                                                                              AAW38633 standard, protein, 193 AA.
S. pneumoniae LPLC protein.
W09743303-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human nucleoplasmin (Npm2) protein.
WO2003091400-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ63172 standard; protein; 214 AA.
                                                                                                                                                                                      20-NOV-1997.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BAYU ) BAYLOR COLLEGE MEDICINE. (AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAYU ) BAYLOR COLLEGE MEDICINE. (AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-2003.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                      COLORY INCYTE PHARM INC.

12 Match 5.8%;

14 Local Similarity 24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-2002.
A (CHIR-) CHIRON SPA.
Query Match
                                      24-APR-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 1281
                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
RESULT 1284
                                                                           Query Match
Best Local Similarity
RESULT 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ70414 standard; protein; 1704 AA.
Human heat mitochondrial protein as a therapeutic target SeqID2220,
WO2003087768-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL61289 standard; protein; 1704 AA.
Human ATP-binding cassette subfamily A (ABC1) member 3 protein.
W02004020583-A2.
11-MAR-2004.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                          AAW46761 standard; protein; 1684 AA.
AAW46761 standard; protein; 1684 AA.
Amino acid sequence of human ATP binding cassette transporter.
WO9748797-A1.
24-DEC-1997.
(GENZ ) GENZYME CORP.
                                                                                                                                                                                                           Query Match

Best Local Similarity 20.3%; Score 69.5; DB 2; Length 1684;

BESULT 1269

ID AAW46771 standard; protein; 1704 AA.

DE Amino acid sequence of human ATP binding cassette transporter.

PN W09748797-A1.
                                                                         Length 1684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8%; Score 69.5; DB 5; Length 1704; 20.3%; Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                            Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 69; DB 4; Length 191;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADK16543 standard; protein; 178 AA.
Nanoarchaeum equitans cancer-associated (CA) protein #247.
Nano2003093434-A2.
13-NOV-2003.
(DIVE-) DIVERSA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 178
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP52094 standard; protein; 1704 AA.
Homo sapiens ABC transporter ABCA3 protein SEQ ID NO:46.
EP1217066-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB09274 standard; protein; 154 AA.
Alloicocccus otitis antigenic protein SEQ ID NO:3214
WO2003048304-A2.
12-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAUG5589 standard; protein; 191 AA.
Propionibacterium acnes immunogenic protein #26485.
WO200181581-A2.
                                                                         Score 69.5; DB 2;
Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 69.5; DB 2; 20.3%; Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%; Score 69.5; DB 8; 20.3%; Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 69.5; DB 7;
Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8;
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 5.8%; Score 69; Local Similarity 27.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM62108 standard; protein; 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.8%;
Best Local Similarity 20.3%;
RESULT 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%;
                                                                         Query Match 5.8%;
Best Local Similarity 20.3%;
RESULT 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMHP ) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                                                                                         24-DEC-1997.
(GENZ ) GENZYME CORP.
                                        23-JAN-1997.
(GENZ ) GENZYME CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2002.
(UYGE-) UNIV GENT.
   hABC3 protein.
WO9702346-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPNE
                                                                                                                                                                                                                                                                                                                                                                                                                                      PADAGE
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AABI6020 standard; protein; 388 AA.
E. coli proliferation associated protein sequence SEQ ID NO:378.
WO200044906-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69; DB 3; Length 509; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 69; DB 3; Length 520;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.8%; Score 69; DB 3; Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG31959 standard; protein; 609 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 38469.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG42138 standard; protein; 508 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 52514.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGG4118 standard, protein; 509 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 25.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABBS9760 standard; protein; 593 AA.
Drosophila melanogaster polypeptide SEQ ID NO 6072.
                                                                                                                                                                                                                                                                                                                                                                                                             ABU14818 standard; protein; 388 AA. Protein encoded by Prokaryotic essential gene #345. WO200277183-A2.
                                                                                                                                                                                                                                                                   AAG98122 standard; protein; 388 AA.
Escherichia coli protein sequence SEQ ID NO:370.
WO200148209-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 69; DB 4;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 69; DB 3; 20.2%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABO61901 sțandard; protein; 472 AA.
Klebsiella pneumoniae polypeptide segid 8418.
US6610836-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fg. (100) GENOME THERAPEUTICS CORP. 127 Match 5.8%; Score 69; tt Local Similarity 21.3%; Pred. No.
                                                                                                                                                                                                                 Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                         5.8%; Score 69; 27.2%; Pred. No.
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                                                                     Score 69;
Pred. No.
Consensus human hypothalamic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC.
                                   06-MAR-1997.
(CHIR ) CHIRON CORP.
                                                                                                                                                                                                                              Best Local Similarity RESULT 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1299
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(PEKE ) PE CORP NY.
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Best Local Similarity
RESULT 1297
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Best Local Similarity
RESULT 1300
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Best Local Similarity
RESULT 1301
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Best Local Similarity
RESULT 1302
ID ABB59760 standard;
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                                                                                  Best Local Similarity
RESULT 1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAN97221 standard; peptide; 370 AA.

Human pituitary-derived G protein-coupled receptor protein.
300858962-A1.
(TAKE) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 69; DB 8; Length 370;
21.8%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 370; 70;
                                                                                                                                                                                                                                                            Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 370; 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGG25539 standard; protein; 370 AA.
Human CRH releasing protein related protein SEQ ID NO: 46.
WO200135984-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABPBISEO standard; protein; 370 AA. Human G protein-coupled receptor 10 protein SEQ ID NO:245. WO200261087-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Length 370
                                                                                                                                                                                                                                                                                                                                                                                                      Length 370;
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                                                                                                                 Length 356
                             AAGO4120 standard, protein; 356 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 27.
EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG04119 standard; protein; 370 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 26
EP1033405-A2.
                                                                                                                                                                                                                                                                                                              AAW31379 standard; protein; 370 AA.
Human G protein-coupled receptor protein from phGR3.
WO970436A2.
10-JUL-1997.
(TAKE) TAKEDA CHEM IND LTD.
ery Match
by Match Similarity 21.8%; Pred. No. 70;
                                                                                                                                                              AAR91218 standard; protein; 370 AA.
Human pituitary G-protein coupled receptor protein.
WO9605302-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
70;
                                                                                                   LUCLY MATCH 5.8%; Score 69; DB 3; Best Local Similarity 21.0%; Pred. No. 66; RESULT 1286
                                                                                                                                                                                                                                                          5.8%; Score 69; DB 2;
21.8%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW95181 standard; peptide; 370 AA.
Human G-protein coupled rceptor polypeptide.
WO9849295-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
70;
         65;
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ID AAM97221 standard; peptide: 370 %
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 21.8%; Pred. No.
RESULT 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69;
Pred. No.
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Pred. No.
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         20.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AD029365 standard; protein; 370 AA.
Human GPCR GPR10, SEQ ID NO:466.
WO2004040000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW27510 standard; protein; 380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-2002.
(LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%;
                                                                                                                                                                                                                          22-FEB-1996.
(TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-1998.
(TAKE ) TAKEDA CHEM IND LTD.
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RESULT 1287
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Best Local Similarity
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         Best Local Similarity
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RESULT 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAY-2004.
(PRIM-) PRIMAL INC.
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Query Match

Query Match

Length 388;

DB 6; 75;

Length 388;

DB 4; 75;

DB 3; Length 388; 75;

Query Match

Best Loca RESULT 1288

A D D E D

Length 380;

DB 2; 73;

DB 7; Length 472; 98;

Length 508;

Length 593;

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5.8%; Score 69; DB 4; Length 666; 23.4%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                 Length 641;
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Pred. No. 2.3e+02;
                                                                                                      Length 624;
                                                                                                                                                                                                                                                                                                                                                                         Length 659;
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Pred. No. 1.6e+02;
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Pred. No. 2e+02;
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human putative spliceosome associated protein (SAP) #52. US2003068803-A1.
                               AAG31958 standard; protein; 624 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 38468.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB42779 standard; protein; 792 AA.
Human ORFX ORF2543 polypeptide sequence SEQ ID NO:5086.
WO200058473-A2.
                                                                                                                                                                                                                                                                                          ABB11769 standard; peptide; 666 AA.
Human dJ37C10.3 ATPase homologue, SEQ ID NO:2139.
WO200157188-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 69; DB 4; I
23.4%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                              5.8%; Score 69; DB 4; 122.7%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 69; DB 3; 21.0%; Pred. No. 1.6e+02;
21.0%; Pred. No. 1.4e+02;
                                                                                                    5.8%; Score 69; DB 3; 21.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP62960 standard; protein; 875 AA.
Human polypeptide SEQ ID NO 397.
WO200218424-A2.
                                                                                                                                                        AAE05101 standard; protein; 641 AA. Drosophila melanogaster dmKSNF. WO200149848-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM79751 standard; protein; 666 AA.
Human protein SEQ ID NO 3397.
WO200157190-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF05168 standard; protein; 681 AA.
Bacterial polypeptide #1281.
US6605709-B1.
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(GENO-) GENOME THERAPEUTICS CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 5.8%;
Best Local Similarity 24.8%;
RESULT 1312
                                                                                                                                                                                                             12-JUL-2001.
(GENO-) GENOPTERA LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-OCT-2000.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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Best Local Similarity
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Best Local Similarity
                                                                                                                     Best Local Similarity RESULT 1305
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAR-2002.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REED/) REED R. (ZHOU/) ZHOU Z.
                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000.
                                                                                    06-SEP-2000.
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RESULT 1313
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AD057686 standard; protein; 227 AA.
Actinobacillus actinomycetemcomitans immunogenic polypeptide #68
WO2004045499-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA14398 standard; protein; 278 AA.
Mouse spermatogenesis related protein sequence SEQ ID NO:140.
WO2003068969-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EBST Local Similarity 40.7%; Score 68.5; DB 3; Length 218; Best Local Similarity 40.7%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 68.5; DB 7; Length 178; 30.7%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 209;
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                                                                                                 Length 1933;
                                                                                                                                                                                                                                                     Length 5127;
                                                                                                                                                  ADM68764 standard; protein; 5127 AA.
Peregrinus maidis ryanodine receptor protein SEQ ID NO:8.
WO2004027042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG25640 standard, protein; 218 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 29784.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG53747 standard; protein; 218 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 68458.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG53772 standard; protein; 218 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 68492.
EP1033405-A2.
6-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vuery Match 5.7%; Score 68.5; DB 5;
Beet Local Similarity 21.8%; Pred. No. 36;
RESULT 1317
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                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                   Score 69; DB 5; I
Pred. No. 6.9e+02;
ABB90877 standard; protein; 1933 AA.
Herbicidally active polypeptide SEQ ID NO 88.
W0200210210-A2.
(FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
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Best Local Similarity 24.3%; Pred. No. 41;
RESULT 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7%; Score 68.5; I
18.2%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 68.5; 1
40.7%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABJ01003 standard; protein; 209 AA.
Human breast specific protein SEQ ID NO:
WO200240672-A2.
                                                                                                                                                                                                                                                                                                       ADM85829 standard; protein; 178 AA.
Enterococcus faecalis polypeptide #309.
US6617156-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF07413 standard; protein; 225 AA. Bacterial polypeptide #3526. US6605709-B1. I2-AUG-2003. (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                 5.8%;
                                                                                                                                                                                                                                                                                                                                                                                      (DOUC/) DOUCETIE-STAMM L A. (BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAY-2002.
(DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-2004.
(UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1318
                                                                                                            Best Local Similarity
RESULT 1314
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RESULT 1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        09-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                         Query Match
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DB 2; Length 383;

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5.7%; Score 68.5; I
                                                             ABUG1817 standard; protein; 383 AA.
Rat-edg.
US6518414-B1.
     (MACL/) MACLENNAN A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2001.
(COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1998.
(UNSY ) UNIV SYDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1337
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Best Local Similarity
RESULT 1336
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Best Local Similarity
RESULT 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
   PA (MACL/) MACLENNAN A
Query Match
Best Local Similarity
RESULT 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-199
                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                              ABB99751 standard; protein; 327 AA.
Amino acid sequence of bacteriophage phiCpnl antigenic protein.
WO200295413-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID ABU29281 standard; protein; 322 AA.

DE Protein encoded by Prokaryotic essential gene #14808.

DE MO20027183-A2.

DE 03-0CT-2002.

PA (ELIT.) ELITRA PHARM INC.

S.7%; Score 68.5; DB 6; Length 322;

Best Local Similarity 30.7%; Pred. No. 66;
                                   DB 6; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                t (CSIR ) COMMONWEALTH SCI & IND RES ORG.
Query Match
5.7%; Score 68.5; DB 4; Length 377;
Best Local Similarity 29.3%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 68.5; DB 8; Length 382; 19.8%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                  DB 6; Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 369,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW87791 standard; protein; 383 AA.
Rat-edg, G-protein coupled receptor superfamily member.
USS856443-A.
05-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 68.5; DB 2;
19.8%; Pred. No. 84;
PD 21-AUG-2003.

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

Query Match 5.7%; Score 68.5; D

Best Local Similarity 29.2%; Pred. No. 54;

RESULT 1323
                                                                                                                                                                                                                                                       WCZUCZ-
28-NOV-2002.
(UYBR-) UNIV BRITISH COLUMBIA.
S.7%; Score 68.5; D
sery Match 5.7%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2000.
(SMIK ) SMITHKLINE BEECHAM CORP.
5.7%; Score 68.5; D
ery Match 5.7%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 30-WAR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 23.3%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                 5.7%; Score 68.5;
18.8%; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY87506 standard; protein; 369 AA.
Human G coupled-protein receptor, GPR10.
WO200017641-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW01664 standard; protein; 383 AA.
p(rat-edg), G-protein coupled receptor.
US5585476-A.
                                                                                                                                                                                                                                                                                                                                             AAWZ5926 standard, protein, 354 AA.
Xenopus melatonin receptor MEL-1Aa.
W99704094-A1.
(6-FEB-1997.
(ADIR ) ADIR & CIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AD029286 standard; protein; 382 AA.
Mouse GPCR EDG1, SEQ ID NO:387.
W02004040000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB28521 standard; protein; 382 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse EDG1 polypeptide. WO200059529-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-DEC-1996.
(MACL/) MACLENNAN A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1326
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1330
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RESULT 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-2004.
(PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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AA002941 standard; protein; 431 AA.
Angiotensin converting enzyme (ACEV) splice variant protein #41.
WO200136632-A2.
PD 11-FEB-2003.

PA (MACL) MACLENNAN A J.

S.7%; Score 68.5; DB 7; Length 383;
Best Local Similarity 19.8%; Pred. No. 84;

RESULT 1333

ID ABG07020 standard; protein; 404 AA.
                                                                                                                                                                                                                                                   5.7%; Score 68.5; DB 4; Length 404; 22.4%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                        (MEDI-) MEDICAL RES COUNCIL.

(MEDI-) MEDICAL RES COUNCIL.

5.7%; Score 68.5; DB 4; Length 411;

(ery Match

7.7%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.7%; Score 68.5; DB 4; Length 431; Best Local Similarity 29.9%; Pred. No. 99; RESULT 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-2003.
(GRNO-) GENOME THERAPEUTICS CORP.
(GRNO-) GENOME THERAPEUTICS CORP.
5.7%; Score 68.5; DB 6; Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 68.5; DB 7; Length 417; 23.2%; Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW88344 standard; protein; 430 AA.
Salmonella enterica O antigen pathway flippase protein.
WO9850531-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 68.5; DB 2; 23.6%; Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 68.5; I
18.8%; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis polypeptide #1597.
US6617156-B1.
                                                                                                    Novel human diagnostic protein; 404 AA.

Novel human diagnostic protein #7011.
W0200175067-A2.
11-CCT-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB71866 standard; protein; 444 AA.
Human CRF1 seven transmembrane domain.
WO200109328-A1.
08-PEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA33815 standard; protein; 437 AA. Acinetobacter baumannii protein #976.
US6562958-B1.
                                                                                                                                                                                                                                                                                                                        AAB68619 standard; protein; 411 AA.
Human PAC 1 receptor isoform 30.
WO200107478-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR88409 standard, protein, 420 AA.
High-affinity melatonin receptor.
WO9535320-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADH87117 standard; protein; 417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MASS-) MASSACHUSETTS GEN HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DOUC/) DOUCETTE-STAMM L A. (BUSH/) BUSH D.
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29.9%; Pred. No. 1e+02;

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Best Local Similarity RESULT 1349
  Query Match S.7%; Score 68.5; DB 4; Length 444; Best Local Similarity 23.7%; Pred. No. 1e+02; RESULT 1341
                                                                                                                                                                                                                                                                                                               5.7%; Score 68.5; DB 5; Length 444; 23.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-2002.

(SALK ) SALK INST BIOLOGICAL STUDIES.

Query Match
5.7%; Score 68.5; DB 6; Length 444;
Best Local Similarity 23.7%; Pred. No. le+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 68.5; DB 7; Length 444; 23.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

ery Match

5.7%; Score 68.5; DB 7; Length 447;

cimilarity 23.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.7%; Score 68.5; DB 6; Length 444; Best Local Similarity 23.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.7%; Score 68.5; DB 6; Length 444; Best Local Similarity 23.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.7%; Score 68.5; DB 8; Length 444;
Best Local Similarity 23.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7%; Score 68.5; DB 2; Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1343

ID ABU08081 standard; protein; 444 AA.

DE Human corticotropin-releasing factor receptor 2 (CRF-R2)

PN US6495343-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ65810 standard; protein; 444 AA.
Human corticotropin-releasing factor receptor CRF-RA2
US2004039173-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AARS8668 standard; protein; 448 AA.
Human PACAP receptor type 1A mature protein.
EP618291-A2.
                                                                                                                                                                                                                                                                                                                                                                           ABR43052 standard; protein; 444 AA.
Human CRH-R1 beta protein SEQ ID NO:2.
WO2003024990-A2.
                                                                              AAE26685 standard; protein; 444 AA.
Human CRF-RA2 splice variant protein.
US2002055617-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE62734 standard; protein; 444 AA.
Human Protein P34998, SEQ ID NO 8667.
WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-NOV-2002.
(SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SALK ) SALK INST BIOLOGICAL STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1344

ID ABG76402 standard; protein; 444 AA.
DE Human hCRP-RA1, splice variant.
PN US6408-B1.
PD 19-NOV-2002.
PA (SALK ) SALK INST BIOLOGICAL STUDIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1347
ID ADC86255 standard; protein; 447 AA.
DE Human GPCR protein SEQ ID NO:708.
PN EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2003.
(UYTE-) UNIV TENNESSEE RES CORP.
(MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-1994.
(TAKE ) TAKEDA CHEM IND LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                         (PERR/) PERRIN M H.
(CHEN/) CHEN R.
(LEWI/) LEWIS K A.
(VALE/) VALE W W.
(DONA/) DONALDSON C J.
(SAWC/) SAWCHENKO P.
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                        09-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                             RESULT 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1346
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ABP65829 standard; protein; 495 AA.
Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:573.
BP1277152-A1.
31-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MEDI-) MEDICAL RES COUNCIL.
5.7%; Score 68.5; DB 4; Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                             02-JNN-2003.
(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
217 Match 5.7%; Score 68.5; DB 7; Length 468;
3f Local Similarity 29.9%; Pred. No. 1.1e+02;
                                                                                                           Length 468;
                                                                                                                                                                                                                                                                                          Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 468
                                                                                                                                                                       ID AMB71874 standard; protein; 468 AA.

BE Human PACR seven transmembrane domain.

PN W0200109328-A1.

PD 08-FEB-2001.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match

Best Local Similarity 29.9%; Pred. No. 1.1e+02;

RESULT 1351

ID ADC86185 standard; protein; 468 AA.

DE Human GPCR protein SEQ ID NO:638.
ABB56380 standard; protein; 468 AA.
Non-endogenous human GPCR protein, SEQ ID NO: 553.
WO200177172-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Luery Match
5.7%; Score 68.5; DB 2;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 05-OCT-1994.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 5.7%; Score 68.5; DB 2;

Query Match 5.7%; Pred. No. 1.1e+02;

RESULT 1354

ID AARS8671 standard; protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-1994.
(TAKE) TAKEDA CHEM IND LTD.
LETY MATCh 5.7%; Score 68.5; DB 2;
LETY MATCh 5.7%; Pred. No. 1.1e+02;
                                                                                  PA (AREN') ARENA PHARM INC.

Query Match
5.7%; Score 68.5; DB 4;
BEST Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68.5; DB 5;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68.5; DB 8;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- AARSB670 standard; protein; 475 AA.
Human PACAP receptor type 1-B2 mature protein.
EP618291-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AARS8669 standard; protein; 476 AA.
Human PACAP receptor type 1B mature protein.
EP618291-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR58671 standard; protein; 476 AA.
Human PACAP receptor type 1C mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD029153 standard; protein; 468 AA.
Human GPCR ADCYAPIRI, SEQ ID NO:254.
WO2004040000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB68618 standard; protein; 524 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-1994.
(TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEST ) SOC PROD NESTLE SA.

117 Match 5.7%;
12 Local Similarity 28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PAC 1 receptor. WO200107478-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-2004.
(PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP618291-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          02-JAN-2003
                                                                    18-OCT-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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(ULSCA) OLISEN H S. (PISCA) PISCHER C L. (ERE) EBNER R. (MOOR.) BREWER L A. (MOOR.) MOORE P A. (SHIY) SHI Y. (LAFL) LAFLEUR D W. (LIYY) LI Y. (ZENG.) ZENG Z. (KYAW.) KYAW H.
                                                                                                                                                                                                                                                                                                                                                                                                                                       HU J.
FLORENCE K A.
                                                                                                                                                                                                                                                                                                    BEDNARIK D P.
ENDRESS G A.
                     EBNER R.
BREWER L A.
MOORE P A.
SHI Y.
LAFLEUR D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1367
                                                                                                                                     Query Match
Best Local Similarity
RESULT 1365
                                                                                                                                                                                                                                                                                                                                                NI J.
FENG P.
YOUNG P. E.
GREENE J M.
FERRIE A M.
         PISCHER C L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 1366
                                                                                                                                                                                                                                           RUBEN S M.
ROSEN C A.
SOPPET D R.
CARTER K C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-2003.
(SUGE-) SUGEN INC.
                                                                                             (LIYY/) LI Y.
(ZENG/) ZENG Z.
(KYAW/) KYAW H.
                                                                                                                                                                                                                                18-SEP-2003
(RUBE/) RUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                 (SHIY/)
(LAFL/)
                                                                                                                                                                                                                                                            (ROSE/)
(SOPP/)
                                                                                                                                                                                                                                                                                                     (BEDN/)
(ENDR/)
(YUGG/)
(NIJJ/)
                                                                                                                                                                                                                                                                                          CART/)
                                                                                                                                                                                                                                                                                                                                                                                                        (FERR/
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FLOR/
                                                                                                                                                                                                                                                                                                                                                                              XOUN/
                                                                                                                                                                                                                                                                                                                                                                                              GREE/
                                                                                                                                                                                                                                                                                                                                                                                                                                       HUJJ/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                       MESOLI 13918

MESOLI 13918

DE ADMISSE standard; protein; 525 AA.

DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:276.

DN WO2003042661-A2.

PD 22-MAY-2003.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

QUERY MATCH

Best Local Similarity 29.9%; Pred. No. 1.3e+02;

RESULT 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABO34523 standard; protein; 548 AA.
Region of human secreted protein encoded by cDNA sequence #150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD 11-JUL-2002.

PA (ELIT-) ELITRA PHARM INC.

Query March 5.7%; Score 68.5; DB 5; Length 541;

Best Local Similarity 21.7%; Pred. No. 1.4e+02;

RESULT 1363
                                                                                    PD 05-0CT-1994.

PA (TAKE) TAKEDA CHEM IND LTD.

QUELY MATCh 5.7%; Score 68.5; DB 2; Length 525;

Best Local Similarity 29.9%; Pred. No. 1.3e+02;

RESULT 1359
                                                                                                                                                                                                                                                                           Score 68.5; DB 6; Length 525;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.7%; Score 68.5; DB 6; Length 525; Beet Local Similarity 29.9%; Pred. No. 1.3e+02; RESULT 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%; Score 68.5; DB 5; Length 548; 34.0%; Pred. No. 1.4e+02;
                                                                                                                                                           ABU08611 standard; protein; 525 AA.
Human pituitary adenylate cyclase (PAC) 1 receptor.
US2002182729-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP7395 standard; protein; 541 AA.
Candida albicans essential protein SEQ ID NO 7832.
WO200253728-A2.
                                                                                                                                                                                                                                                                                                                    ABPB1873 standard; protein; 525 AA.

Human PACAP receptor type 1 protein SEQ ID NO:231.

WO200261087-A2.

08-AUG-2002.

(LIFE-) LIFESPAN BIOSCIENCES INC.
Best Local Similarity 29.9%; Pred. No. 1.3e+02; RESULT 1358
                                 AARS8659 standard; protein; 525 AA.
Human PACAP receptor type 1A protein.
EP618291-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG95329 standard; protein; 548 AA.
Human novel secreted protein #150.
US6420526-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUL-2002.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                              5.7%;
                                                                                                                                                                                                      05-DEC-2002.
(DICLY) DICICCO-BLOOM E.
(NICO/) NICOT A.
(LUNN/) LU N.
(SUHJ/) SUH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NI J.
FENG P.
YOUNG P.
GREENE J M.
FERRIE A M.
DUAN D R.
HU J.
FLORENCE K A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOPPET D R. CARTER K C. BEDNARIK D P. ENDRESS G A.
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
RESULT 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RUBEN S M.
ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003049618-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUJJ/) H
(FLOR/) 1
(OLSE/) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ROSE/)
(SOPP/)
(CART/)
(BEDN/)
(ENDR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GREE/)
(FERR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XOUN/)
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ADH17089 standard, protein, 548 AA. Human translation initiation factor eIF3 p66 subunit protein. WO2003097854-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 68.5; DB 8; Length 548; 34.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) 05-OCT-1994.

(TAKE) TAKEDA CHEM IND LTD.

Query Match 5.7%; Score 68.5; DB 2; Length 552;

Best Local Similarity 29.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 548;
5.7%; Score 68.5; DB 6; Length 548; 34.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 04-DEC-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match
Beet Local Similarity 34.0%; Pred. No. 1.4e+02;
RESULT 1368

ID ARRS661 standard; protein; 552 AA.

DE Human PAGAP receptor type 1-B2 protein.

PN EP618291-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%; Score 68.5; DB 7; 34.0%; Pred. No. 1.4e+02;
                                                                       ADI23184 standard; protein; 548 AA.
Novel human secreted protein seg id 469.
US2003175858-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AARS8662 standard; protein; 553 AA.
Human PACAP receptor type 1C protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH74186 standard; protein; 548 AA. Human secreted protein #150. US2003225248-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP618291-A2.
05-OCT-1994.
(TAKE ) TAKEDA CHEM IND LTD.
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PD 15-NOV-2001.

PA (CROP-) CROPDESIGN NV.

QUERY MATCH

Best Local Similarity 22.3%; Pred. No. 2e+02;

RESULT 1381
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PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 5.7%; Score 68.5; DB 7; Length 738;

Best Local Similarity 20.3%; Pred. No. 2.1e+02;

RESULT 1382
                                                                                                                                                                           5.7%; Score 68.5; DB 3; Length 724; 22.3%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.7%; Score 68.5; DB 4; Length 788; Best Local Similarity 19.2%; Pred. No. 2.3e+02; RESULT 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 890;
                                                      AAG20244 standard; protein; 724 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 22357.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-2000.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
(CREA-) CREATOGEN GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68.5; DB 3;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 68.5; DB 3; 23.8%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68.5; DB 3;
Pred. No. 2.7e+02;
   22.3%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC95469 standard; protein; 738 AA.
E. faecium protein sequence SEQ ID 5096.
US6583275-B1.
                                                                                                                                                                                                                                                            AAU72535 standard; protein; 724 AA.
Arabidopsis cell cycle protein CCP25.
W0200185946-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human WFS1 mutant P504L.
WQ200018787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY92103 standard; protein; 885 AA.
Human WFS1 mutant DELSO8 YVYLL.
WO200018787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY92110 standard; protein; 890 AA.
Human WFS1 polymorphism 1333V.
WO200018787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY92105 standard; protein; 890 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB46310 standard; protein; 788 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H. pylori HPS115 protein.
WO200073502-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIW ) UNIV WASHINGTON. (PERM/) PERMUTT M A. (INOU/) INOUE H. (MUEC/) MUECKLER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIW ) UNIV WASHINGTON. (PERM/) PERMUTT M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ob-AFK-2000.
(UNIW ) UNIV WASHINGTON.
(PERM/) PERMUTT M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human WFS1 mutant G695V. WO200018787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                      Best Local Similarity RESULT 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PERM/) PERMUTT M A.
   Best Local Similarity RESULT 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INOU/) INOUE H. (MUEC/) MUECKLER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MUEC/) MUECKLER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INOU/) INOUE H
                                                                                                                                                      06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABUSO927 standard; protein; 691 AA.
Helicobacter pylori selected interacting domain (SID) protein #270.
WO200266501-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-2004.

(ELIT-) ELITRA CANADA LTD.

(RLIT-) ELITRA CANADA LTD.

3-7%; Score 68.5; DB 8; Length 597;

Best Local Similarity 26.2%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-2002.
(BLIT-) BLITRA PHARM INC.
(ery Match 5.7%; Score 68.5; DB 6; Length 634;
(ery Match 26.3%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSTARR-2003.
(GENO-) GENOME THERAPEUTICS CORP.
(GENO-) GENOME THERAPEUTICS CORP.
5.7%; Score 68.5; DB 7; Length 660;
   Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 68.5; DB 3; Length 704;
                                                                                                                                                                                                                                    5.7%; Score 68.5; DB 2; Length 553; 29.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 5.7%; Score 68.5; DB 4; Length 588; Best Local Similarity 19.6%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 68.5; DB 5; Length 670; 22.1%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP98892 standard; protein; 597 AA.
C. albicans specific gene, orf6.4254, protein sequence.
WO2004056965-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG20246 standard; protein; 663 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 22359.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG20245 standard; protein; 704 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 22358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                April 2018 
                                                                                                                                                                                                                                                                                                      Human GABA transporter homologue, SEQ ID NO:2075. WO200157188-A2.
   5.7%; Score 68.5; DB 2; 29.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 68.5; DB 3; 22.3%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%; Score 68.5; DB 5;
19.2%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO81139 standard; protein; 660 AA.
Pseudomonas aeruginosa polypeptide #13314.
US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.7%; Score 68.5
                                                                  AAR58660 standard; protein; 553 AA.
Human PACAP receptor type 1B protein.
EP618291-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB53933 standard; protein; 670 AA.
Lactococcus lactis protein kupl.
FR2807-446-Al.
12-OCT-2001.
                                                                                                                                                                        05-OCT-1994.
(TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jar.

J. thalit.

J. P. 200.

J. Match

Best Local Similarity 2.

RESULT 1376

ID ABB5393 standar

DE Lactococcur

PN FR28074

PD 12.

PA
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
RESULT 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1375
ID AAG20240
DE Arabidop
PN EP103340
PD 06-SEP-2
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RESULT 1374

Best Loca RESULT 1372

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Best Local Similarity 19.8%; Pred. No. 4e+02;
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Query Match 5.7%; Score 68.5; DB 7; Length 1178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.7%; Score 68.5; DB 5; Length 894; Best Local Similarity 22.9%; Pred. No. 2.7e+02; RESULT 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7%; Score 68.5; DB 3; Length 937; 23.8%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 68.5; DB 3; Length 890; 23.8%; Pred. No. 2.7e+02;
                                          5.7%; Score 68.5; DB 3; Length 890; 23.8%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                        Score 68.5; DB 3; Length 890;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB70303 standard; protein; 1178 AA.
C. neoformans amino acid sequence SEQ ID NO:3347.
WO2003052076-A2.
26-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Score 68.5; DB 5; 22.9%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                    5.7%; Score 68.5; DB 3; 23.8%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP20153 standard; protein; 894 AA.
Streptococcus polypeptide SEQ ID NO 5482.
WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP29861 standard; protein; 894 AA.
Streptococcus polypeptide SEQ ID NO 8898.
WO200234771-A2.
                                                                                        AAY92109 standard; protein; 890 AA. Human WFS1 polymorphism R456H. WO200018787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY92102 standard; protein; 937 AA.
Human WFS1 mutant de1882fs/ter937.
WO200018787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY92104 standard; protein; 890 AA.
Human WFS1 mutant P724L.
WO200018787-A1.
                                                                                                                                                                                                                                                                                          AAY92100 standard; protein; 890 AA.
WFS1 polypeptide.
WO200018787-A1.
                                                                                                                                                                                                                                    Best Local Similarity 23.8%;
RESULT 1388
                                                                                                                                               06-APR-2000.
(UNIW) UNIV WASHINGTON.
(PERM/) PERMUTT M A.
(INOU/) INOUE H.
(MUEC/) MUECKLER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-2000.
(UNIW) UNIV WASHINGTON.
(PERW) PERMUTT M A.
(INOW) INOUE H.
(MUEC/) MUECKLER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2002.
(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 02-MAY-2002.

1 (CHIR-) CHIRON SPA.

1 (GENO-) INST GENOMIC RES.

Query Match 5.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIW) UNIV WASHINGTON. (PERM/) PERMUTT M A. (INOU/) INOUE H. (MUEC/) MUECKLER M.
                                                                                                                                                                                                                                                                                                                                                              (UNIW ) UNIV WASHINGTON.
(PERM/) PERMUTT M A.
(INOU/) INOUE H.
(MUEC/) MUECKLER M.
5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
1389
         (INOU/) INOUE H. (MUEC/) MUECKLER M.
                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2000
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RESULT 1390
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RESULT
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pp 14-JAN-1999.

PA (USSH) US DEPT HEALTH & HUMAN RESOURCES.

Query Match
Best Local Similarity 25.8%; Pred. No. 4.6e+02;

RESULT 1395

ID AAB30730 standard; protein; 3015 AA.

MO200075338-A2.

PA WOZO0075338-A2.
                                                                                                                                                                                                                                                                                                             Length 3015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3015,
                                                                                                                                                                                                                                                                                                                                                                               AAB30732 standard, protein, 3015 AA.
Amino acid sequence of chimeric Hepatitis C virus clone J6S.
WQ200075338-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OB-JAN-2004.
(CALY ) CALIFORNIA INST OF TECHNOLOGY.
(CALY ) CALIFORNIA INST OF TECHNOLOGY.
5.7%; Score 68; DB 8; Length 273;
cery Match
5.7%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 20-JUN-2001.

PA (KYOW) KYOWA HAKKO KOGYO KK.

Query Match 5.7%; Score 68; DB 4; Length 247;

Best Local Similarity 23.1%; Pred. No. 52;

RESULT 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wuery match 5.7%; Score 68; DB 8; Length 200; Best Local Similarity 23.5%; Pred. No. 39; RESULT 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADK16845 standard; protein; 200 AA.
Nanoarchaeum equitans cancer-associated (CA) protein #398.
Nay0103034344-A2.
13-NOV-2003.
(DIVE-) DIVERSA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB78946 standard; protein; 247 AA.
C. glutamicum SRT protein sequence SEQ ID NO:152.
W0201108044A2.
(BADI ) BASF AG.
                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
ry Match
t Local Similarity 26.7%; Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 14-DEC-2000.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

Query March

5.7%; Score 68.5; DB 4;

Best Local Similarity 26.7%; Pred. No. 1.5e+03;

RESULT 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE21323 standard; protein; 273 AA.
Mouse MrgBlO (mas-related gene) protein.
W200193555-A2.
08-NOV-2001.
(CALY ) CALIFORNIA INST OF TECHNOLOGY.
5 7%; Score 68; DB 5; St Local Similarity 26.1%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%; Score 68; DB 2; 23.0%; Pred. No. 56;
AAW88448 standard; protein; 1296 AA.
Caenorhabditis elegans NPC1 protein orthologue.
WO9901555-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGG1355 standard; protein; 247 AA.
AG11camicum protein fragment SEQ ID NO: 5109.
EP1108790-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 68; 23.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY41212 standard; protein; 258 AA.
E. coli MttB polypeptide.
W09951753-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH08589 standard; protein; 273 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1999.
(UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1401
                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
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Truncated cysLT2 cysteinyl leukotreine receptor (HG57). WO200142269-A1.
                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1414
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1415
                                                                                                                               Best Local Similarity
RESULT 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1420
                                                                             (GDOW/) O'DOWD B. (GEOR/) GEORGE S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
RESULT 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB82852 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200168842-A2.
20-SEP-2001.
(FARB ) BAYER AG.
                                                                                                                     Match
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2002.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
5.7%; Score 68; DB 6; Length 330;
ery Match 5.7%; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYCOCT-2002.
(BRIM) BRISTOL-MYERS SQUIBB CO.
ery Match
5.7%; Score 68; DB 6; Length 308;
ery --- cimilarity 29.5%; Pred. No. 71;
                                                                                                                  Length 293,
                                                                                                                                                                                                                                                                             Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68; DB 3; Length 330;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGI7029 standard; protein; 330 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 17896.
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG42139 standard; protein; 330 AA.
Arabidopsis thaliana protein fragment SEQ ID NO: 52515.
EP1033405-A2.
RESULT 1403

ID ABUll963 standard; protein; 293 AA.

DB Human HGPRBMY11 C-terminal deletion mutant M1-G293.

DD 31-OCT-2002.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

Query Match

5.7%; Score 68; DB 6; Leng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABUI1962 standard; protein; 308 AA.
Human HGPRBMY11 N-terminal deletion mutant E23-V330
WO200286123-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68; DB 5;
Pred. No. 78;
                                                                                                                                                                                                                                                                              DB 4;
67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68; DB 3;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 5.7%; Score 68; DB 7;
Local Similarity 28.3%; Pred. No. 67;
                                                                                                                                                                                                                                                                                         Best Local Similarity 26.0%; Pred. No. 67; RESULT 1405
DD ADMOSCH standard; protein; 295 AA.
DB Human protein of the invention SEQ ID NO:4304
PN BP1347046-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABUI1900 standard; protein; 330 AA.
Human G-protein coupled receptor HGPRBMY11.
WO200286123-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG77964 standard; protein; 330 AA.
Human G-protein coupled receptor PFI-017.
08-NOV-2001.
(HARL/) HARLAND L.
                                                                                                                                                                                                                                                                           5.7%; Score 68; 26.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 68; 20.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA35057 standard; protein; 309 AA. Acinecobacter baumannii protein #2218. US6562958-B1. 13-MAY-2003: (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                AAG80106 standard; protein; 295 AA.
Human CCR1 protein.
WO200172830-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB85097 standard; protein; 331 AA
                                                                                                                                                                                                                                                                                                                                                                                  24-SEP-2003.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%;
                                                                                                                                                                                                                   (1PFP-) IPF PHARM GMBH. (FORS/) FORSSMANN U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Best Local Similarity
RESULT 1407
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Best Local Similarity
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Best Local Similarity
RESULT 1409
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                             Query Match
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
RESULT 1410
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ABREE

PP PE

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25-MAY-2001.
(AREN-) ARENA PHARM INC.
5.7%; Score 68; DB 4; Length 346;
                                                                                                                                                                                                                         Length 341;
                                                                            Length 331;
                                                                                                                                                                                                                                                                                                                                                                           Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68; DB 4; Length 346;
Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 346;
                                                                                                                            AAE07539 standard; protein; 341 AA.
Human G-protein coupled receptor 1b (GPCR1b) variant.
W0200159113-A2.
16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE07538 standard; protein; 346 AA.
Human G-protein coupled receptor la (GPCR1a) variant.
WO200159113-A2.
                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PA (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

Query Match

5.7%; Score 68; DB 5;

Best Local Similarity 20.2%; Pred. No. 83;

RESULT 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                       5.7%; Score 68; DB 4; 29.5%; Pred. No. 82;
                                                                        5.7%; Score 68; DB 4;
29.5%; Pred. No. 79;
                                                                                                                                                                                                                                                                           ABUI1939 standard; protein; 341 AA.
Human G-protein coupled receptor HGPRBMY11v2.
WO200286123-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU07294 standard; protein; 346 AA.
Cysteinyl leukotriene receptor HIPHUM0000007
WO200159105-A1.
                                                                                                                                                                                                                                                                                                                             31-CCT-2002.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
(ery Match
5.7%; Score 68; DB
(ery Match
7.1%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68; DB
Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU04368 standard; protein; 346 AA.
Human G-protein coupled receptor, hRUP14.
WO200136471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                        ABP25610 standard; protein; 344 AA.
Streptococcus polypeptide SEQ ID NO 396.
WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.7%; Score 68; Best Local Similarity 29.5%; Pred. No. RESULT 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Score 68; 29.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human LTC4 receptor SEQ ID NO: 2. WOZO0119986-Al.
14-JUN-2001.
(UYVI-) UNIV VIRGINIA PATENT FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (YAMA ) YAMANOUCHI PHARM CO LTD. (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 5:7%;
Ouery Match 5:7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.5%;
RESULT 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human P2Y-like GPCR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-AUG-2001.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
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ABB05229 standard; protein; 346 AA.
Human LTD4-like G protein-coupled receptor protein SEQ ID NO:2.
WO200194580-A1.
                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.

5.7%; Score 68; DB 4; Length 346;

3t Local Similarity 29.5%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 346;
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 5; Length 346; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 68; DB 5; Length 346; 29.5%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 346;
                                                                                                                         5.7%; Score 68; DB 4; Length 346; 29.5%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68; DB 5; Length 346;
Pred. No. 84;
                                AAU04383 standard; protein; 346 AA.
Human G-protein coupled receptor, hRUP14, mutant L246K.
WO200136471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU10004 standard; protein; 346 AA.
Human CysLT2-like G-protein coupled receptor protein
WO200177149-A2.
                                                                                                                                                                              AAE08553 standard; protein; 346 AA.
Human G-protein coupled receptor (GPCR)-like protein
WO200159118-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
84;
                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE17231 standard; protein; 346 AA.
Human CysLT2 GPCR (G-protein coupled receptor)
WO200192302-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 68; DB 5; 29.5%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2001.
(INCYTE GENOMICS INC.
5.7%; Score 68; DB
Best Local Similarity 29.5%; Pred. No. 84;
29.5%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                      AAE12022 standard; protein; 346 AA.
Human G-protein coupled receptor, GCREC-1.
WO200172836-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG77965 standard; protein; 346 AA.
Human G-protein coupled receptor PFI-017*.
US2001039037-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 68; 29.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP95624 standard; protein; 346 AA. Human GPCR polypeptide SEQ ID NO 58. WO200216548-A2. 28-FEB-2002. (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG66684 standard; protein; 346 AA.
Human novel polypeptide #19.
WO200244340-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-25-2001.
(MERE ) MERCK PATENT GMBH.
(ery Match 5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2001.
(REGE-) REGENERON PHARM INC.
                                                                                       25-MAY-2001.
(AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 1425
                                                                                                                                      Best_Local Similarity RESULT 1422
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Best Local Similarity
RESULT 1426
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Best Local Similarity
RESULT 1427
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1428
                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-2002.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2001.
(HARL/) HARLAND L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FARB ) BAYER AG.
Query Match
                                                                                                                                                                                                                                         16-AUG-2001
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1424
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ABPB1707 standard; protein; 346 AA.
Human cysteinyl leukotriene CYSLT2 receptor protein SEQ ID NO:589.
WO200261087-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL96534 standard, protein; 346 AA.
Human mutant G protein-coupled receptor (GPCR) polypeptide #2.
US2003166148-A1.
                                                                                              (BRIM ) BRISTOL-MYERS SQUIBB CO.

5.7%; Score 68; DB 6; Length 346;

st Local Similarity 29.5%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 68; DB 7; Length 346; 29.5%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length 346;
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68; DB 7; Length 346; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 346;
                                                                                                                                                                                                                                                                           Length 346;
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Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL96460 standard; protein; 346 AA.
Human G protein-coupled receptor (GPCR) polypeptide #7.
US2003166148-A1.
04-SEP-2003.
                                                                                                                                                                                                                                                                                                                                      ADH00945 standard; protein; 346 AA.
Human cysteinyl leukotriene (CysLT2)-like GPCR protein
US2003157541-A1.
                                                                                                                                                                                                                                                                             DB 6;
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 7;
Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.7%; Score 68; DB 8; 29.5%; Pred. No. 84;
RESULT 1430

ID ABU11923 standard; protein; 346 AA.

DB Human G-protein coupled receptor HGPRBMY11v1.

PD W0200286123-A2.

PD 31-OCT-2002.

PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68;
Pred. No.
                                                                                                                                                                                                                                  08-AUG-2002.
(LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.7%; Score 68;
Best Local Similarity 29.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK51004 standard; protein; 346 AA.
Human NOV6B protein sequence SeqID24.
WO2003083046-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK51002 standard; protein; 346 AA.
Human NOV6A protein sequence SeqID22.
WO2003083046-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADG25233 standard, protein; 346 AA. Human CysLT2 receptor variant. US2003203833-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG25220 standard; protein; 346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 29.5%;
FESULT 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.7%;
Best Local Similarity 29.5%;
RESULT 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CysLT2 receptor US2003203833-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LOWI/) LOWITZ K P.
Query Match
Best Local Similarity
RESULT 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A (CHEN/) CHEN R.
A (DANG/) DANG H T.
A (LOWIT) LOWITZ K P.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1438
                                                                                                                                   Best Local Similarity RESULT 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IGNA/) IGNAR D M. (PILL/) PILLAI S.
                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2003.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-2003
                                                                                                                         Query Match
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Human chemokine receptor-1 (CKR-1) polypeptide

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DB 8; Length 346;
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 4; Length 347; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                DB 8; Length 346;
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.7%; Score 68; DB 8; Length 346;
29.5%; Pred. No. 84;
                                                                                                                                                                                         Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 5.7%; Score 68; DB 2; Length 355; Local Similarity 26.0%; Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 355;
87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB85094 standard; protein; 347 AA.
Human cysLT2 cysteinyl leukotreine receptor (HG57).
WO200142269-A1.
                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 29-JUL-1997.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
QUESTY MATCH 5.7%; Score 68; DB 2;
Best Local Similarity 26.0%; Pred. No. 87;
RESULT 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68; DB 3;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB20571 standard; protein; 355 AA.
Human CC-chemokine receptor 1 (CCR1) protein.
WO200044790-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW25751 standard; protein; 355 AA.
Human MIP-1alpha/RANTES receptor protein.
JP09176048-A.
                                                  Score 68;
Pred. No.
                                                                                                                                                                                     Query Match 5.7%; Score 68;
Best Local Similarity 29.5%; Pred. No.
RESULT 1440
                                                                                                                                                                                                                                                                                                                             5.7%; Score 68; 29.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 08-JUL-1997.

PA (TAKE) TAKEDA CHEM IND LTD.

QUELY MATCh 5.7%; Score 68;
Best Local Similarity 26.0%; Pred. No.
                                                                                          AUM91891 Standard; protein; 346 AA.
Novel human protein NOV35b.
WO2003102159-A2.
11-DEC-2003.
3TV MAICA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                           AD029277 standard; protein; 346 AA.
Human GPCR CYSLT2, SEQ ID NO:378.
WO2004040000-A2.
                                                                                                                                                                                                                                    A ADM41889 standard; protein; 346 AA.
A ADM41889 standard; protein; 346 AA.
Novel human protein NOV35a.
NOV03102159-A2.
11-DEC-2003.
Ouery Match
5.7%; Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYVI-) UNIV VIRGINIA PATENT FOUND. (DDOW) O'DOWD B. (GEOR/) GEORGE S R. 5.7%. Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW26588 standard; protein; 355 AA.
Human MIP-1 alpha/RANTES receptor.
US5652133-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU09082 standard; protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR52749 standard; protein; 355 AA C-C chemokine receptor.
                                                5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-1994.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000.
(LEUK-) LEUKOSITE INC.
                                                Query Match
Best Local Similarity
RESULT 1439
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-2004.
(PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
              (IGNA/) IGNAR D M. (PILL/) PILLAI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9411504-A1.
30-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Si
RESULT 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Human soft tissue sarcoma-upregulated protein - SEQ ID 4344 WO2004048938-A2.
                                                    Length 355;
                                                                                                                                                                                      Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 355;
87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 68; DB 8; Length 355; 26.0%; Pred. No. 87;
                                                                                                                                                                                                                                                                                                                         Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 355;
                                                                                                                                                                                                                                                                                                                                                               ADF76506 standard; protein; 355 AA.
Novel human secreted and transmembrane protein SeqID 180.
WO2003072035-A2.
                                                                                      Amino acid sequence of human chemokine receptor CCR1.
WO2003014153-A2.
                                                                                                                                                                                                                                                     Human C-C chemokine receptor 1 protein SEQ ID NO:62.0200261087-A2.
08-AUG-2002.
(LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                     DB 6;
87;
                                                                                                                                                  PD 20-FEB-2003.

PA (TOPI-) TOPIGEN PHARM INC.

QUETY MATCh 5.7%; Score 68; DB 6;

Best Local Similarity 26.0%; Pred. No. 87;

RESULT 1449
                                                    . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 8;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB 8;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP88568 standard; protein; 355 AA.
Human chemokine (C-C) motif receptor 1 CCR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
87;
                                                  Score 68; DB
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.7%; Score 68; Best Local Similarity 26.0%; Pred. No. RESULT 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match
Best Local Similarity 26.0%; Pred. No.

RESULT 1456
                                                                                                                                                                                                                                                                                                                       5.7%; Score 68; 26.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1453
ID AD019490 standard; protein; 355 AA.
DE Human PRO polypeptide #210.
PN W02004043361-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO polypeptide #211.
27-Mav.-^..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO16838 standard; protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AD029119 standard; protein; 355 AA.
Human GPCR CCR1, SEQ ID NO:320.
W02004040000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ21524 standard, protein, 355 AA.
                                                                                                                                                                                                                                     ABP81790 standard; protein; 355 AA
US2003uru-
23-JAN-2003.
(SCHE ) SCHERING CORP.
5.7%; S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHEMOCENTRYX INC.
CHEMOCENTRYX INC.
3.7%;
Anilarity 26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 26.0%;
RESULT 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCR1 amino acid sequence. WO2003047420-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                      04-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAY-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-2004.
(PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1450
                                                    Query Match
Best Local Similarity
RESULT 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUN-200;
(CHEM-) CHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Protein encoded by Prokaryotic essential gene #17047. WO200277183-A2. 03-OCT-2002.
                                                                                                              ADP88570 standard; protein; 355 AA.
Human macrophage inflammatory protein-1-alpha/RANTES receptor.
WO2004052186-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN47559 standard; protein; 389 AA.
Thermococcus kodakaraensis KOD1 protein sequence SeqID1437
WO2004022736-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 6; Length 393;
Pred. No. 1e+02;
                                                             Score 68; DB 8; Length 355; Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                         Score 68; DB 6; Length 357;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.7%; Score 68; DB 7; Length 365; 21.8%; Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 68; DB 4; Length 372;
Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 365; 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 373
                                                                                                                                                                                                            Length 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU50321 standard; protein; 393 AA.
Protein encoded by Prokaryotic essential gene #35848
WO200277183-A2.
                                                                                                                                                                                                                                                               ABU44640 standard; protein; 357 AA.
Protein encoded by Prokaryotic essential gene #30167.
W020027183-A2.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOME THERAPEUTICS CORP.

ry Match
5.7%; Score 68; DB 7;
t Local Similarity 22.4%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 68; DB 8;
21.8%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB58017 standard; protein; 372 AA.
Drosophila melanogaster polypeptide SEQ ID NO
W0200171042-A2.
                                                                                                                                                                                                          Score 68; DB 8;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC99421 standard; protein; 373 AA.
B. faecium protein sequence SEQ ID 7048.
US6583275-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                              ADD46815 standard; protein; 365 AA.
Rat Protein BAA03912, SEQ ID NO 12501.
WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD46813 standard; protein; 365 AA.
Rat Protein BAA03912, SEQ ID NO 12499.
WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-2004.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU31520 standard; protein; 395 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 21.6%;
RESULT 1465
ID ABU3150 ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%;
21.1%;
                                                               5.7%;
                                                                                                                                                                                                            5.7%;
                                                                                                                                                                                                                                                                                                                                                       y Match 5.7%;
Local Similarity 23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                            24-JUN-2004.
(FORS-) FORSYTH INST.
                                                (FORS-) FORSYTH INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1461
                                                                              Best Local Similarity
RESULT 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
           WO2004052186-A2.
24-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-200
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Si
RESULT 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1462
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ABUS2686 standard; protein; 446 AA.
Human signal transduction-associated protein from DKF2phfbr2_2c17.
WO200112659-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD 22-FEB-2001.

PA (GEHU-) GERMAN HUMAN GENOME PROJECT.

Query Match

5.7%; Score 68; DB 4; Length 446;

Best Local Similarity 27.4%; Pred. No. 1.2e+02;

RESULT 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.7%; Score 68; DB 4; Length 426; 24.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 446;
                                                                                                                                                                                                                                                                                    Length 414;
                                                                                                                                                    Length 396;
                 Length 395;
                                                     ADO2027/183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB64152 standard; protein; 426 AA.
Drosophila melanogaster polypeptide SEQ ID NO 19248.
WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68; DB 5; I
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                   26-AUG-2003.
(GENO-) GENOME THERAPEUTICS CORP.
(GENO-) GENOME THERAPEUTICS CORP.
5.7%; Score 68; DB 7; I
cry Match
5.7%; Score 68; DB 7; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; DB 4;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68; DB 2;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68; DB 3;
Pred. No. 1.2e+02;
                  DB 6;
1e+02;
                                                                                                                                                Score 68; DB 6;
Pred. No. 1e+02;
                                                                                                                                                                                                 ABO64352 standard; protein; 414 AA.
Klebsiella pneumoniae polypeptide segid 10869.
US6610836-Bl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-2002. (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                    Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                  AAY05501 standard, protein, 426 AA.
Bacillus subtilis metalloprotease YHFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP60125 standard, protein, 450 AA.
Human epilepsy related protein 49.50.
CN1345812-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO 2513.
WO200153312-A1.
26-JUL.2001.
IY MAtch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR67692 standard; protein; 471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY99670 standard; protein; 446 AA.
Human GTPase associated protein-21.
WO200031263-A2.
                                                                                                          WOZUGE...
03-007-2002.
(ELIT-) ELITRA PHARM INC.
GAT MATCH 5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WOZUCCZ--
02-JUN-2000.
(INCY-) INCYTE PHARM INC.
5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.3%;
(ELIT-) ELITRA PHARM INC.

ry Match 5.7%;
t Local Similarity 21.4%;
                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1999.
(GEMV ) GENENCOR INT INC.
(GEMV ) GENENCOR INT BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1474
                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1471
                               Best Local Similarity RESULT 1466
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          WO9914341-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                        Query Match
                                                                                                                                                                                                                                                                                                                      RESULT 1468
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM36457 standard; protein; 472 AA.
Propionibacterium acnes predicted ORF-encoded polypeptide #1133
WO2003033515-A1.
                                                                                                                                                                                                                                                                                DEPOSED

1 (TRAI) TAKARA SHUZO CO LID.

Query Match

5.7%; Score 68; DB 2; Length 471;

Query Match

5.7%; Pred. No. 1.36+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.7%; Score 68; DB 4; Length 472; Best Local Similarity 19.4%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 68; DB 4; Length 485; 27.4%; Pred. No. 1.3e+02;
                                                                          Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 68; DB 6; Length 472; 19.4%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 488;
                                                                                                                                                                                                                                                                                                                                                                                         Length 471;
                                                                                                                                                     Aureobasidin sensitivity regulatory gene caaurl product.
EP692534-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP73191 standard; protein; 471 AA.
Candida albicans essential protein SEQ ID NO 7028.
WO200253728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB56384 standard; protein; 488 AA.
Non-endogenous human GPCR protein, SEQ ID NO: 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. 19139918 standard; protein; 472 AA. Propionibacterium acnes immunogenic protein #834. WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                         MOLOULE
23-AUCOL.
(ELIT-) ELITRA PHARM INC.
(ELIT-) ELITRA PHARM INC.
5.7%; Score 68; DB 4; L
5.7%; Pred. No. 1.3e+02;
                            AU3-5-2-004.
01-DEC-1994.
(TAXI ) TAXARA SHUZO CO LID.
(TAXI ) TAXARA SHUZO CO LID.
5.7%; Score 68; DB 2; I
6ry Match
5.7%; Score 68; DB 2; I
7.30+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDEC-1994.
01-DEC-1994.
(TAXI ) TAKARA SHUZO CO LID.
(TAXI ) TAKARA SHUZO CO LID.
5.7%; Score 68; DB 2; I
ery Match
5.7%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 68; DB 5; I
25.4%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW02271 standard; protein; 488 AA.
Human prostaglandin receptor BP2.
W09506664-A1.
09-MAR-1995.
(MERI ) MERCK PROSST CANADA INC.
(MERI ) MATCH
5 7%; Score 68; DB 2; 1
5t Local Similarity 26.8%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR67696 standard; protein; 472 AA.
C. albicans caauri gene product.
AU9463129-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM41154 standard; protein; 485 AA. Human polypeptide SEQ ID NO 6085. WO20015313-A1. 26-JUL-2001. (HYSE-) HYSEQ INC.
                                                                                                                                 AAR88133 standard; protein; 471 AA
C. albicans caaurl gene product.
AU9463129-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 25.49
RESULT 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1482
                                                                                    Best Local Similarity RESULT 1475
                                                                                                                                                                                                                                                Best Local Similarity RESULT 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1483
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2225
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ADN40008 standard; protein; 488 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C378.
WO2003042661-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR57071 standard; protein; 490 AA.
Baboon/macaque prostaglandin E2 receptor EP4 protein SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 519;
                                                                                                                                                                                                                                 Length 488;
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.7%; Score 68; DB 7; Length 490; Best Local Similarity 26.8%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 488;
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                                                                                                                 ABP81905 standard; protein; 488 AA.
Human prostaglandin E receptor EP4 protein SEQ ID NO:296.
WO200261087-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH11546 standard; protein; 490 AA.
Chimpanzee prostaglandin E2 receptor EP4 subtype, SEQ
EP125897-A1.
26-MAR.-2003.
(PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU37983 standard, protein; 542 AA.
Protein encoded by Prokaryotic essential gene #23510.
                                                                                                                                                                                                                                                                    ID AA030984 standard; protein; 488 AA.

DE Human prostaglandin E receptor (EP4) protein.

PD 26-JUN-2003.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 5.7%; Score 68; DB 6; I Best Local Similarity 26.8%; Pred. No. 1.38+02;

RESULT 1486
                                                                                                                                                                         PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
QUELY MATCh 5.7%; Score 68; DB 6; I
Best Local Similarity 26.8%; Pred. No. 1.38+02;
RESULT 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 68; DB 7; I
26.8%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%; Score 68; DB 8;
26.8%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68; DB 6; Pred. No. 1.4e+02;
                                                   Score 68; DB 4;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NORQ ) HOKKO CHEM IND CO LTD.
(NORQ ) NORINSUISANSHO NOGYO KENKYU.

5.7%; Score 68; DB 2;
t Local Similarity 24.1%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW70285 standard; protein; 519 AA.
Oryza sativa RNA polymerase sigma factor.
JP10201475-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG26292 standard; protein; 490 AA.
Novel human diagnostic protein #26283.
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD029622 standard; protein; 488 AA.
Human GPCR PTGER4, SEQ ID NO:724.
WO2004040000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAY-2003.
(EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%;
PD 18-OCT-2001.

PA (AREN-) ARENA PHARM INC.

QUELY MACCh

Best Local Similarity 26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 19-MAR-2003.

PA (PFIZ ) PFIZER PROD INC.

QUETY MATCH

BEST LOCAL SIMILATITY 26.8%;

RESULT 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-2004.
(PRIM-) PRIMAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
RESULT 1488
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RESULT 1487
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Best Local Similarity
RESULT 1489
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-1998
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ADPO6233 standard; protein; 542 AA.
Noisseria meningitidis MCS8 OMV-related membrane protein - SBQ ID 116.
WO2004046177-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.7%; Score 68; DB 3; Length 717; Best Local Similarity 28.3%; Pred. No. 2.38+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oueray March
S.7%; Score 68; DB 5; Length 562;
Query March
Best Local Similarity 30.6%; Pred. No. 1.64+02;
RRSULT 1496
ID AAU72956 standard; protein; 562 AA.
DE Neisseria meningitidis virulence protein #46.
PN WO20185772-A2.
PN WO20185772-A2.
PD 15-NOV-2001.
PA (MICR-) MICROSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 68; DB 5; Length 664; 19.3%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%; Score 68; DB 4; Length 714; 28.4%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Section (1972) National Section 1970 National Section 1970 National Section 1970 National Section 1970 National Section National National Section National N
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(ACTI-) ACTIVE PASS PHARM INC.
(ACTI-) ACTIVE PASS PHARM INC.
5.7%; Score 68; DB 5; Length 646;
ery Match 5.7%; Score 68; DB 5; Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 68; DB 5; Length 562; 30.6%; Pred. No. 1.6e+02;
03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
5.7%; Score 68; DB 6; Length 542;
ery Match 5.7%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                 5.7%; Score 68; DB 8; Length 542; 30.6%; Pred. No. 1.6e+02;
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Human ORPX ORF1583 polypeptide sequence SEQ ID NO:3166.
W020058473-A2.
05-OCT-2000.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB71668 standard; protein; 714 AA.
Drosophila melanogaster polypeptide SEQ ID NO 41796.
27-SEP-2001.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE Herbicidally active polypeptide SEQ ID NO 1317.

DE Herbicidally active polypeptide SEQ ID NO 1317.

DE HERB-2002.

PA (FEB-2002.

PA (FARB) BAYER AG.

Query Match

Best Local Similarity 19.3%; Pred. No. 2.1e+02;

RESULT 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU72948 standard; protein; 562 AA.
Neisseria meningitidis virulence protein #38.
WO200185772-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU72914 standard; protein; 562 AA.
Neisseria meningitidis virulence protein #4.
WA20018572-A2.
(MICR-) MICROSCIENCE LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE28968 standard; protein; 646 AA. Human ABCG4 transporter protein #2. WO200270691-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-2001.
(MICR-) MICROSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 3
RESULT 1497
ID AAE28968 standard; pro
DE Human ABCG4 transporte
PD 12-SEP-2002.
PA (ACTI-) ACTIVE PASS PH
                                                                     Query Match
Best Local Similarity 3
RESULT 1493
RESULT 169283 standard; pro
DE Neisseria meningitidis
PN WOZOGY466177-A2.
PD 03-UN-2004.
PA (CHIR ) CHIRON SRL.
                                                                                                                                                                                                                                                                                                        PD 03-JUN-2004.
PA (CHIR) CHIRON SRL.
Query Match
Best Local Similarity 3
RESULT 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1498
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Best Local Similarity
RESULT 1500
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RESULT 1495
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